

00722724.120400

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TCACGGCTCCGGTCAGCTCTCGTTCCGAGAAGCACCGCGCTGGCGTCCGGCCATCCCGGGGAATCGGC
CCCCCTCTGACCTAGTGTTCGCGGGGCAAAAAGGGTCTTCCCGGGCTCGCTCGTGCAGGGGCCAT
TTGGGCGCCCTGAGCGCGGGCGTGGAGCCCTTGGAGCCCGCCCGAGCAGGGGGCACACCCGGAACCG
CCCTGAGCGCCCGGGACCATGACCGGGAGGCCATCTGAGCGCCCTGCCACCATTCCTTACCA
CAAACTGCGCGACCTGCGCTACCTGAGCCCGGGCGCTCTGGCACTGTGTGCTCCCGCCCGCACG
TAGACTGGCGCGTCCAGGTGGCCCTGAAGCACCTGCACATCCACACTCCGCTGCTGCACAGTGAA
AGAAAGCATGTCTTAAGAGAAGCTCAAAATTTTACACAAAGCTAGATTAGTTACATTCCTTCCAAT
TTTGGGAATTTGCAATGAGCGCTCAATTTTGGGAATAGTACTGAATACATGCCAAATGCAATCAT
TAAATGAACCTCTACATAGGAAAACCTCAATATCCTGATGTTGCTTGGCCATTGAGATTTCTATC
CTGCATGAAATTCGCCCTTGGTGTAAATTACCTGCACAATATGACTCCTCCTTTACTTCATCATGA
CTTTAGACTCAGAATATCTTTTGCACAATGTTTCAATGTTTGAATTCAGATTTTGGTTTAT
CAAGTGGCGCATGATGTCCCTCTCACAGTCACGAAGTAGCAAACTCTGCACGAGAAGGAGGACAC
ATTATCTATATGCCACCTGAAAACTATGAACCTGGACAAAAATCAAGGGCCAGTATCAAGCACGA
TATATATAGCTATGCAGTTATCACATGGGAAGTGTATCCAGAAAACAGCCCTTTTGAAGATGTCA
CCAATCCTTTGCAGATAATGTATAGTGTGTACACAGGACATCGACCTGTTATTAATGAAGAAAGT
TTGCCATATGATATACCTCACCCAGCACGTATGATCTCTCTAATAGAAAGTGGATGGGCACAAAA
TCCAGATGAAAGACCATCTTTCTTAAAAATGTTTATAGAACTTCAACCAAGTTTTCAGAACATTTG
AGAGATAACTTTCTTGAAGCTCTTATTCAGCTAAAGAAAAACAAGTTACAGAGTGTCTTCAAGT
GCCATTACCTATGTGACAGAAGAAAAATGGAATTTCTCTCAACATACCTGTAATCATGGTCC
ACAAGAGGAATCATGTGGATCTCTTCAGCTCCATGAAAAATAGTGGTTCTCTGAAACTTCAAGGT
CCCTGCCAGCTCCTCAAGACAAATGATTTTATCTAGAAAAGCTCAAGACTGTCTTATTTATGAAG
CTGCATCACTGTCTCTGGAAATCACAGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATT
CTGTGATCACAAAGACCATTTCTATGCTCTTTCAGCAATTAATAATCCACTCTCAACTGCAGGAAACT
CAGAACGTCTGCAGCCTGGTATAGCCCGAGCAGTGGATCCAGAGCAAAAAGGGGAAGACATTGTGAAC
CAAAATGACAGAAGCCTGCCCTTAACCAAGTCGCTAGATGCCCTTCTGTCCAGGGGACTTCAATCATGAA
AGAGGACTATGAACCTGTTAGTACCAAGCCCTACAAGGACCTCAAAAGTCAGACAAATTAAGACA
CTACTGACATCCAAAGGAGAAGAAATTTGCCAAAGTTTATAGTACAAAAATGAAAGATTAACAAACAA
ATGGGTCTTTCAGCCTTACCCGAAATACTTGTGGTTTCTAGATCACCATCTTAAATTTACTTCA
AAATAAAAGCATGTAAGTGACTGTTTTTCAAGAAGAAATGTGTTTCATAAAAGGATATTTATAAA
AA (SEQ ID NO:1)

FIG. 1

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Met	Asn	Gly	Glu	Ala	Ile	Cys	Ser	Ala	Leu	Pro	Thr	Ile	Pro	Tyr	His	Lys	Leu	Ala	Asp	20
Leu	Arg	Cys	Leu	Ser	Arg	Gly	Ala	Ser	Gly	Thr	Val	Ser	Ser	Ala	Arg	His	Ala	Asp	Tyr	40
Arg	Val	Gln	Val	Ala	Val	Lys	His	Leu	His	Ile	His	Thr	Pro	Leu	Leu	Asp	Ser	Gln	Arg	60
Lys	Asp	Val	Leu	Arg	Glu	Ala	Gln	Ile	Leu	His	Lys	Ala	Arg	Phe	Ser	Tyr	Ile	Leu	Pro	80
Ile	Leu	Gly	Ile	Cys	Asn	Glu	Pro	Glu	Phe	Leu	Gly	Ile	Val	Thr	Glu	Tyr	Met	Pro	Asn	100
Gly	Ser	Leu	Asn	Glu	Leu	Leu	His	Arg	Lys	Thr	Glu	Tyr	Pro	Asp	Val	Ala	Thr	Pro	Leu	120
Arg	Phe	Arg	Ile	Leu	His	Gln	Ile	Ala	Leu	Gly	Val	Asn	Tyr	Leu	His	Asn	Met	Thr	Pro	140
Pro	Leu	Leu	His	His	Asp	Leu	Lys	Thr	Gln	Asn	Ile	Leu	Leu	Asp	Asn	Gln	Phe	His	Val	160
Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ser	Lys	Trp	Arg	Met	Met	Ser	Leu	Ser	Gln	Ser	Arg	Ser	180
Ser	Lys	Ser	Ala	Pro	Glu	Gly	Gly	Thr	Ile	Ile	Tyr	Met	Pro	Pro	Glu	Asn	Tyr	Gln	Pro	200
Gly	Gln	Lys	Ser	Arg	Ala	Ser	Ile	Lys	His	Asp	Ile	Tyr	Ser	Tyr	Ala	Val	Ile	Thr	Trp	220
Gln	Val	Leu	Ser	Arg	Lys	Gln	Pro	Phe	Glu	Asp	Val	Thr	Asn	Pro	Leu	Gln	Ile	Met	Tyr	240
Ser	Val	Ser	Gln	Gly	His	Arg	Pro	Val	Ile	Asn	Glu	Glu	Ser	Leu	Pro	Tyr	Asp	Ile	Pro	260
His	Arg	Ala	Arg	Met	Ile	Ser	Leu	Ile	Gln	Ser	Gly	Trp	Ala	Gln	Asn	Pro	Asp	Gln	Arg	280
Pro	Ser	Phe	Leu	Lys	Cys	Leu	Ile	Gln	Leu	Glu	Pro	Val	Leu	Arg	Thr	Phe	Gln	Gln	Ile	300
Thr	Phe	Leu	Glu	Ala	Val	Ile	Gln	Leu	Lys	Lys	Thr	Lys	Leu	Gln	Ser	Val	Ser	Ser	Ala	320
Ile	His	Leu	Cys	Asp	Lys	Lys	Lys	Met	Glu	Leu	Ser	Leu	Asn	Ile	Pro	Val	Asn	His	Gly	340
Pro	Gln	Glu	Glu	Ser	Cys	Gly	Ser	Ser	Gln	Leu	His	Glu	Asn	Ser	Gly	Ser	Pro	Gln	Thr	360
Ser	Arg	Ser	Leu	Pro	Ala	Pro	Gln	Asp	Asn	Asp	Phe	Leu	Ser	Arg	Lys	Ala	Gln	Asp	Cys	380
Tyr	Phe	Met	Lys	Leu	His	His	Cys	Pro	Gly	Asn	His	Ser	Trp	Asp	Ser	Thr	Ile	Ser	Gly	400
Ser	Gln	Arg	Ala	Ala	Phe	Cys	Asp	His	Lys	Thr	Ile	Pro	Cys	Ser	Ser	Ala	Ile	Ile	Asn	420
Pro	Leu	Ser	Thr	Ala	Gly	Asn	Ser	Gln	Arg	Leu	Gln	Pro	Gly	Ile	Ala	Gln	Gln	Trp	Ile	440
Gln	Ser	Lys	Arg	Glu	Asp	Ile	Val	Asn	Gln	Met	Thr	Gln	Ala	Cys	Leu	Asn	Gln	Ser	Leu	460
Asp	Ala	Leu	Leu	Ser	Arg	Asp	Leu	Ile	Met	Lys	Glu	Asp	Tyr	Glu	Leu	Val	Ser	Thr	Lys	480
Pro	Thr	Arg	Thr	Ser	Lys	Val	Arg	Gln	Leu	Leu	Asp	Thr	Thr	Asp	Ile	Gln	Gly	Glu	Glu	500
Phe	Ala	Lys	Val	Ile	Val	Gln	Lys	Leu	Lys	Asp	Asn	Lys	Gln	Met	Gly	Leu	Gln	Pro	Tyr	520
Pro	Glu	Ile	Leu	Val	Val	Ser	Arg	Ser	Pro	Ser	Leu	Asn	Leu	Leu	Gln	Asn	Lys	Ser	Met	540

(SEQ ID NO:2)

FIG. 2

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TTTTATGGG AATCCGAGCT TGGAGAGAG AGARCAATTC GAGAANTAAA TTTAAATTC
 AGATTTAACC AATGTTGTTT TAAAATATTC TAACTTCAAA GAATGATGCC AGAAGTTTAA
 AAGGAGCTGC GCAGAGTAGC AGGGGCGCTT GAGGGCGCGG CCTGAATCCT GATTGCGCTT
 TTGCTCAGAG GACACAGGCA GCTCAGAGT AATTTCGGAA AAGTAGCGCG TTGCTACTTT
 TACTATGGAA GAGCAGGGCC ACAGTGAGAT GGAATATTC GCATCAGAGT CTCACCCCA
 CATTCAATTA CTGAAAAGCA ATCGGGAAT TTTGGTCACT CACATCCGCA ATACTCAGTG
 TGTGGTGGAC AACTTCTCA AGAATGACTA CTTCTCGGCC GAAGATGCGG AGATTGTGTG
 TCGCTGCCCC ACCCAGCCTG ACAAGGTCCG CAAAATTCTG GACCTGCTAC AGAGCAAGGG
 CGAGGAGGTG TCCGAGTTCT TCTCTACTTT GCTCAGCAA CTGCGAGATG CCTACGTGGA
 GCTCAGGCTT TGGCTGCTGG AGATCGGCTT CTGCGCTTGG CTGCTCACTC AGAGCAAGT
 GCTGCTCAGC ACTGACCCAG TTAGCAGGTA TACCCAGCAG CTGCGACACC ATCTGGGCGG
 TCACTCAGAG TTGCTGCTTT GCTATGCCCA GAAGGAGGAG CTGCTGCTGG AGGAGATCTA
 CATGACACC ATCATGGAGC TGGTGGCTT CAGCAATGAG AGCCTGGCA GCTCAACAG
 CTTGCGCTGC CTGCTGGACC ACACGACCG CATCTCAAT GAGCAGGGTG AGACCATCTT
 CATCTGCGT GATGCTGGGG TGGGCAAGTC CATGCTGCTA CAGCGGCTGC AGAGCCTTGT
 GGGCAGGGGC CGGCTAGAGC CAGGGGTCAA ATTCTTCTTC CACTTTGCTT GCGCGATGTT
 CAGCTGCTTC AAGGAAAGTG ACAGGCTGTG TGTGAGGAC CTGCTCTTCA AGCACTACTG
 CTACCCAGAG CGGACACCCC AGGAGGTGTT TCGCTTCTG CTGCGCTTGC CCGACGTGGC
 CTTCTTCAAC TTGATGGCC TGGACGAGCT GCACTCGGAC TTGACCTCA GCGCGGTGGC
 TACAGCTGC TCGCGCTGG AGCCTGCGCA CCGCGCTGTC TTGCTGGCA ACCTGCTCAG
 TGGGAGGCTG CTGAGGGGG CTAGCAAGCT CTTACAGGCC CCGACAGGCA TTAGGTGCGC
 GCGCCAGTTC CTGCGGAAGA AGGTGCTTCT CCGGGGCTTC TCCCCAGCC ACCTGCGCGC
 CTATGCCAGG AGGATGTTCC CCGAGCGGCG CTTGAGGAC CCGCTGCTGA GCGAGCTGGA
 GGGCAACCCC AACCTCTGCA GCTGTGCTG TGTGCGCTTC TTGCTGGA TCACTCTCGG
 GTGCTTCCAG CACTTGGCTG CTGCGTTTCA AGGCTCACCA CAGCTGCGCG ACTGCAGAT
 GACCTGACA GATGCTTTC TGTGGTCACT TTAGGTCCAT CTGAACAGGA TGCAGCGCG
 CAGCCTGGTG CAGCGGAACA CAGCAGGCC AGTGGAGACC CTCCAGCGCG GCGGGAGAC
 TGTGTGCTGC CTGGGGCAGG TCGCCACCG GGGCATGGAG AAGAGCCTCT TTGTCTTCA
 CGAGGAGGAG GTGCAGGCT CCGGGCTGCA GGAGAGAGAC ATGCAGCTGG GCTTCTGCGG
 GCGTTTGGCG GAGCTGGGCG CCGGGGTGA CCGCAGTCC TATGAGTTT TCGACCTCAG
 GCTCAGGCC TTCTTACAG CTTCTTCTCT CTTGCTGGAC GACAGGGTGG GCACTCAGGA
 GCTGCTCAGG TTCTTCCAGG AGTGGATGCC CCGTGGGGG GCAGCGACCA CTTCTCTCA

FIG. 3 (page 1 of 2)

FIG. 3 (page 2 of 2)

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NEEQCHSEMEIIPSESHPHIQLLKSNRELLTTHIRNTQCLVONLLKNDYFSAEDAEIWCACFTQP
DKVRKILDLVQSKGEEVSEFFLYLLOQLADAYVDLRPWLLLEIGFSPSLLTQSKVWNTDPVSRYT
QQLRHHLGRDSKFVLCIAQKEELLEEITMDTIMELVGFSNESLGSLSLACLDDHTTGILNEQG
ETIFILGDAGVGKSMILLQRLQSLWATGRLDAGVKFFHFRCRMFSCFKESDRLCLQDLLFKHYCY
PERDPEEVFAFLLRFPHVAFITFDGLDELHSELDLSRVPDSSCPWEPAPLVLNLLSGKLLKG
ASKLLTARTGIEVPROFLRKKVLLRGFSFPHLAYARRMFPERALQDRLLSQLEANPNLCSLCSV
PLFCNIIIFRCFQHFRAAFEGSPQLPDCTMTLTDFVLLVTEVHLNRMQPSSSLVQRNTRSPVETLHA
GRDTLCSLGQVAHRGMEKSLFVFTQEEVQASGLQERDMQLGFLRALPELGFGGDQQSIEFFHLTL
CAFFTAFFLVLDLDRVGTQCELLRFFQEWMPFAGAAATTSCYSPFFLPFQCLOGSGPAREDLFANKDHF
QFTNLFLOGLLSKAKQKLLRHLPAAALRRKXKALWAHLFSSLRGYLKSLPRVQVESFNQVQAMP
TFIWMRLCIVETQSQKVGQLAARGICANYLKLTVCNACSADCSALSFVLHHFPKRLALDLNNNL
NDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSEELTKYKIVTYLGLYNNQITDVGARYVTKIL
DECKGLTHLKLGGKNTITSEGGKYLALAVKNSKSISEVGMWGNQVGDGAKAFAEALRNHPSLITL
SLASNGISTEGGKSLARALQQNTSLEILNLTQNEINDEVAESLAEMLKVNQTLKHLWLIQNQITA
KGTALADALQSNITGITEICLNGNLKPEEAKVYEDEKRIICF (SEQ ID NO:8)

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TACGGCTCCGACTTCTGAGAATGACTACTTCTCGGCCAAGATGCGGAGATTGTGT
 TTGCTTCCCCCAGCCAGCCTGACRAGGTCCGCAAAATTCTGGACCTGGTACAGAGCAAG
 GCGGAGGAGGTGTCCGAGTTCTTCTCTACTTGTCTCAGCAACTGCGAGATGCTTACGT
 GGACCTCAGGCCTTGGCTGCTGAGATCGGCTTCTCCCTTCCCTGCTCACTCAGAGCA
 AGTCTGTGGTCAACACTCAGCCAGTGAAGCAGGTATACCCAGCAGCTGCGACACCATCTG
 GCGCTGACTCCAAGTTCTGTCTGTGCTATGCCAGAAGGAGGAGCTGCTGTGAGGA
 TATCTACATGGACACCATCATGGAGCTGGTGGCTTCAGCAATGAGAGCCTGGGCAGCC
 TGAACAGCCTGGCCTGCTTCTGGACCAACCAACGGCATCTCAATGAGCAGGGTGAG
 ACCATCTTCATCCTGGGTGATGCTGGGTGGGCAAGTCCATGCTGCTACAGCGGTGCA
 TAGCCTCTGGGCCACGGGCCGGCTAGACGCAGGGGTCAAATTCTTCTTCCACTTTCGCT
 TCCGCATGTTCAAGTCTTCAAGGAAAGTGACAGGCTGTGTCTGCAGGACCTGCTCTTC
 AAGCACTACTGCTACCCAGAGCGGGACCCGAGGAGGTGTTTGCCTTCTGCTGCGCTT
 CCCCCACGTGGCCCTCTTCACTTTCGATGGCCTGACAGAGCTGCACTCGGACTTGGACC
 TGAGCCGCGTGCCTGACAGCTCTTCCCCCTGGGAGCCTGCCACCCCCCTGGTCTTGTCTG
 GCCAACCTGCTCAGTGGGAAGCTGCTCAAGGGGGCTAGCAAGCTGCTCACAGCCCCGAC
 AGGCATCGAGGTCCCGGCCAGTTCTGCGGAAGAAGGTGCTTCTCCGGGGCTTCTCCC
 TCAGCCACCTGCGGCCCTATGCCAGGAGGATGTTCCCGAGCGGGCCCTGCAGGACCGC
 TTGCTGAGCCAGCTGGAGGCCAACCCCAACCTCTGCAGCCTGTGCTCTGTCCCCCTCTT
 TTGCTGGATCATCTTCCGGTGTCTGCAGCACTTCCGTGCTGCTTTGAAGGCTCACCAC
 AGCTGCCCCACTGCAGGATGACCCCTGACAGATGTCTTCTCTGCTGCTGAGGTCCAT
 CTGAACAGGATGCAGCCCCAGCAGCCTTGTGCGAGCGGAACACAGCAGCCCCGAGAC
 CCTCCACGCGCGGCCGGGACACTGTGTGCTGCTGCGGAGGAGGTGCGCCACCGGGCATGG
 AGAAGAGCCTCTTTGTCTTCAACCCAGGAGGAGGTGCAGGCCCTCCGGGCTGCAGGAGAGA
 GACATGCAGCTGGGCTTCTTCCGGGCTTTGCCGGAGCTGGGCCCCGGGGGTGACCAGCA
 GTCCTATGAGTTTTTCCACCTCAGCCTTCTTCACTGTAAACTGGGATCCAGTATAGA
 CTTTGGAAATCAGTAGACACCATATGCTTCAAAAAACAGGGGCTATTAAATGACATCA
 GGAGCCAGAAAGTCTCATGGCTGTGCTTCTTGAAGTTTATACAAACACAGATCA
 CGATGTCGGAGCCAGACTGGGAAAAAACHAAATAACAAGTGAAGGAGGGAAGTATCTCG
 CCCTGGCTGTGAAGAACAGCAATCAATCTCTGAGGTTGGGATGTGGGGCAATCAAGTT
 GGGGATGAAGGAGCAAAGCCTTCCAGAGGCTCTGCGGAACCAACCCAGCTTGACCAC
 CCTGAGTCTTGGCTCCAACGGCATCTCCACAGAAGGAGGAAAGAGCCTTGGCAGGGCCC
 TGCAGCAGAACAGTCTCTAGAAATACTGTGGCTGACCCAAAATGAATCAACGATGAA
 TTGGCAGAGAGTTTGGCAGAAATGTTCAAAGTCAACCAGAGCTTAAAGCATTATGGCT
 TATCCAGAAATCAGATCAGAGTCTTTTGTGTCAGTGTCTTAAAGGGGCTGCGCAGCGG
 TACTATCAGGAGTCCACTGCCTCATGATGCAAGCCAGCTTCTGTGCAGAGGTCTGG
 TCGGCAAACTCCCTAAGTACCCGCTACAATTCTGCAGAAAAAGAATGTGTCTTGGAGC
 TGTGTAGTTACAGTAAATACACTGTGAAGAGACTTTATTGCCTATTATAATTATTTT
 ATCTGAAGCTAGAGGAATAAAGCTGTGAGCAACAGAGGAGGCCAGCCTCACCTCATTC
 CAACACCTGCCATAGGGACCAACGGGAGCGAGTTGGTCACCGCTCTTTTATTGAAGAG
 TTGAGGATGTGGCACAAGTTGGTGCCAAGCTTCTTGAATAAAACGTGTTTGATGGATT
 AGTATTATACCTGAAATATTTTCTTCTCTCAGCACTTTCCCATGTATTGATACTGGT
 CCCACTTCACAGCTGGAGACACCGGAGTATGTGCAGTGTGGGATTTGACTCCTCCAAGG
 TTTTGTGGAAAGTTAATGTCAAGGAAAGGATGCACCACGGGCTTTTAAATTTAATCCTG
 GAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAGCTCTTAGCTGGTCTAAGA
 ATGACGATGCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTCCTCTGCTAGGCTACCTT
 CCTCTAGAAGGCTGAGTACCATGGGCTACAGTGTCTGGCCTTGGGAAGAAGTATTCTG
 TCCCTCCAAAGAAATAGGGCATGGCTTGGCCCTGTGGCCCTGGCATCCAAATGGCTGCT
 TTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCTGCTTCCCAAGCAGCTGAAG
 GGTGACTAAACGGGGCCCAAGACTCAGGGGATCGGCTGGGAAGTGGGCCAGCAGAGCAT
 GTTGGACACCCCCACCATGGTGGGCTTGTGGTGGGCTGCTCCATGAGGTTGGGGGTGAT
 ACTACTAGATCACTTGTCTCTTGGCAGCTCATTTGTTAATAAAATACTGAAACACAA
 AA
 AAAAAAAAAAAAA (SEQ ID NO:25)

FIG. 5

[illegible]

FIG. 6

[illegible]

FIG. 7

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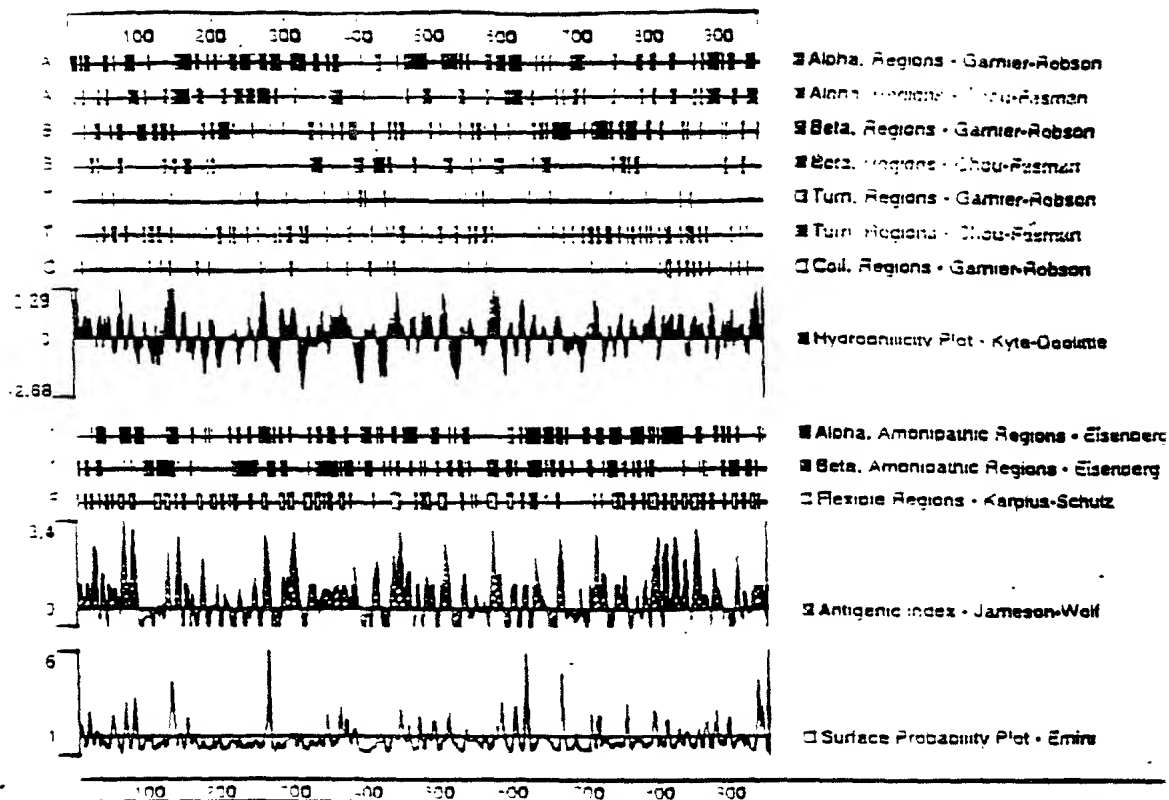


FIG. 8

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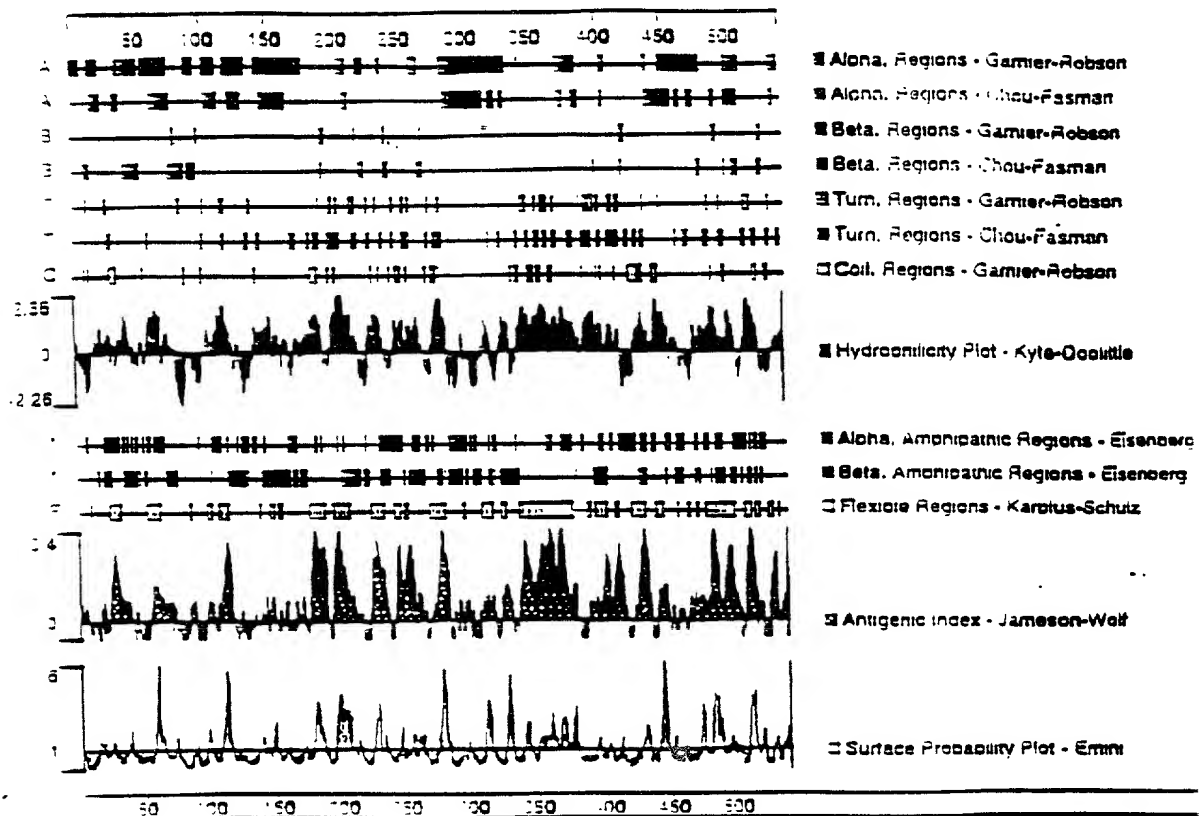


FIG. 9

[illegible]

FIG. 10 (Page 1 of 3)

Variable	Mean	SD	Min	Max
Age	45.2	12.5	25	65
Gender	0.48	0.50	0	1
Marital status	0.65	0.48	0	1
Education	12.5	2.1	9	16
Income	3500	1500	1000	8000
Health status	0.72	0.45	0	1
Exercise frequency	0.35	0.48	0	1
Stress level	0.68	0.42	0	1
Sleep quality	0.55	0.50	0	1
Diet quality	0.62	0.45	0	1
Work-life balance	0.58	0.48	0	1
Family support	0.75	0.42	0	1
Community involvement	0.45	0.50	0	1
Life satisfaction	0.65	0.45	0	1
Overall well-being	0.60	0.48	0	1

FIG. 10 (Page 2 of 3)

GCTTTTAATTTTAATCCTGGAGTCTCACTGTCTGCTGGCAAAGATAGAGAATGCCCTCAG
CTCTTAGCTGGTCTAAGAATGACGATGCCCTTCAAAATGCTGCTTCCACTCAGGGCTTCTC
CTCTGCTAGGCTACCCCTCCTCTAGAAGGCTCAGTACCATGGGCTACAGTGTCTGGCCTTG
GGAAGAAGTGATTCTGTCCCTCCAAAGAAATAGGGCATGGCTTGCCCCCTGTGGCCCTGGC
ATCCAAATGGCTGCTTTTGTCTCCCTTACCTCGTGAAGAGGGGAAGTCTCTTCCTGCCTC
CCAAGCAGCTGAAGGGTGACTAAACGGGCGCCAAGACTCAGGGGATCGGCTGGGAAGTGG
GCCAGCAGAGCATGTTGGACACCCCCCACCATGGTGGGCTTGTGGTGGCTGCTCCATGAG
GGTGGGGGTGATACTACTAGATCACTTGTCTCTTGCCAGCTCATTGTTAATAAAATAC
TGAAAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGG (SEQ ID NO:38)

FIG. 11

CACGCGTCCGCGCTACTSCGGGAGCAGCGTCCTCCCGGGCCACGGCGCTTCCCGGGCCCG
GCGTCCCGGACCATGGCGCTCTCCGGGCTCTTCTCTAGCTCTCAGCGGCTGCGAAGTCT
GTAAACCTGGTGGCCAGTGATTGTAAAGTCAGGAGACTTTCCTTCGGTTTTCTGCCTTTGA
TGGCAAGAGGTGGAGATTGTGGCGGCGATTACAGAAAAACATCTGGGAAGACAAGTTGCTG
TTTTTATGGGAATCGCAGGCTTGGAAAGAGACAGAAGCAATTCCAGAAATAAATTGGAAAT
TGAAGATTTAAACAATGTTGTTTTTAAAAATATTCTAACTTCAAAGAATGATGCCAGAACT
TAAAAAGGGGCTGCGCAGAGTAGCAGGGGGCCCTGGAGGGCGCGGCCTGAATCCTGATTGC
CCTTCTGCTGAGAGGACACACGCAGCTCAAGATGAATTTGGGAAAAGTAGCCGCTTGCTA
CTTTAACTATGGAAGAGCAGGGCCACAGTGAGATGGAAATAATCCCATCAGAGTCTCACC
CCCACATTCAATTACTGAAAAGCAATCGGGAACCTTCTGGTCACTCACATCCGCAATACTC
AGTGTCTGGTGGACAACCTTGTGAAGAATGACTACTTCTCGGCCGAAGATGCGGAGATTG
TGTGTGCCTGCCCCACCCAGCCTGACAAGGTCCSCAAAATTCTGGACCTSGTACAGAGCA
AGGGCGAGGAGGTGTCCGAGTTCTTCTCTACTTGTCTCAGCAACTCGCAGATGCCTACG
TGGACCTCAGGCCTTGGCTGCTGGAGATCGGCTTCTCCCTTCCCTGCTCACTCAGAGCA
AAGTCGTGGTCAACACTGACCCAGGTAGGAGTCAGCCCCAGCAAGACCGCAGGCACCAGT
GCAAGCAGGGCCCTGGGGGTTTTGGTAATGGCTGGGCCAGCCCTGAGTGCCACCTCAGGA
AGCAGGCCCAGGTGCTATTTTGATTTTAGAAAAGGAACAGCTGAATCCTGTCTCCCAAGTG
CAGCCCAGGTGGCTGCGATTGAACTGCCCCACACCTCGATGGTCTGGTTTTATAGAGGGGCC
TTTGGAAGTATGGGAATGGCCTGTGTTCTGACCCCTTGCTTTCTTCTTCTGACATAT
GTAGACATTTTAATGGTTGCACAAATCAAGGTTGTATTTTTTTTTCTTTAAAAAATCT
TTAGCTGGACATGGTAGCACACACCTGTAGTTCCAGCTACTCAGGAGGCTGAGGCAAGAG
GACTGCTTGAGCCCCAGAGTCTAAGGCTGCAGCGAGCTATGATTGTGCCCTACACTCCA
CAGCCTGGGTTTTAGAGTGAGACCCTGTCTCTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAANGGGCGG (SEQ ID NO:40)

FIG. 12

MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL				Majority
10	20	30	40	
MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL				CARD4-Y CLONE
MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL				CARD4-Z CLONE
MEEQGHSEMEIIPSESHPHIQLLKSNRELLVTHIRNTQCL				CARD4L
VDNLLKNDYFSAEDAEIVCACPTQPDKVRKILDLVOSKGE				Majority
50	60	70	80	
VDNLLKNDYFSAEDAEIVCACPTQPDKVRKILDLVOSKGE				CARD4-Y CLONE
VDNLLKNDYFSAEDAEIVCACPTQPDKVRKILDLVOSKGE				CARD4-Z CLONE
VDNLLKNDYFSAEDAEIVCACPTQPDKVRKILDLVOSKGE				CARD4L
EVSEFFLYLLOQLADAYVDLRPWLLEIGFSPSLLTOSKVV				Majority
90	100	110	120	
EVSEFFLYLLOQLADAYVDLRPWLLEIGFSPSLLTOSKVV				CARD4-Y CLONE
EVSEFFLYLLOQLADAYVDLRPWLLEIGFSPSLLTOSKVV				CARD4-Z CLONE
EVSEFFLYLLOQLADAYVDLRPWLLEIGFSPSLLTOSKVV				CARD4L
VNTDPVSRYTQQLRHHLEGRDSKFVLCYAOKEELLLEEIYM				Majority
130	140	150	160	
VNTDPVSRYTQQLRHHLEGRDSKFVLCYAOKEELLLEEIYM				CARD4-Y CLONE
VNTDPGRSOPQDDRRH-----				CARD4-Z CLONE
VNTDPVSRYTQQLRHHLEGRDSKFVLCYAOKEELLLEEIYM				CARD4L
DTIMELVGFSNESLGSLSLACLDDHTTGILNEOXXXX--				Majority
170	180	190	200	
DTIMELVGFSNESLGSLSLACLDDHTTGILNEOAAASR--				CARD4-Y CLONE
-----				CARD4-Z CLONE
DTIMELVGFSNESLGSLSLACLDDHTTGILNEOGETIFI				CARD4L
-----XCKXKXK				Majority
210	220	230	240	
-----KVTG				CARD4-Y CLONE
-----QCKQ				CARD4-Z CLONE
LGDAGVGKSMMLQRLQSLWATGRLDAGVKFFFHFRGRMFS				CARD4L
-----XC-----				Majority
250	260	270	280	
C-----VC-----				CARD4-Y CLONE
-----				CARD4-Z CLONE
CFKESDRLCGLQDLLFKHYCYPERDPPEEVFAFLLRFPHVAL				CARD4L
-----XCKXKXK-----				Majority
290	300	310	320	
-----RTGSSS-----				CARD4-Y CLONE
-----				CARD4-Z CLONE
CTFDGLDELSLSDLSRVPDSSCPWEPAPHPVLNLLSG				CARD4L

FIGURE 14 (1 of 4)

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-----TXXKXKXKXKX-----Majority			
	330	340	350 360
112	-----T T A T Q S S T P R-----		
141	-----T T A T Q S S T P R-----		
161	-----T T A T Q S S T P R-----		
	-----P C-----Majority		
	370	380	390 400
112	-----R C-----		
141	-----R C-----		
161	-----R C-----		
	-----L P X C-----Majority		
	410	420	430 440
124	-----L P S C-----		
141	-----L P S C-----		
161	-----L P S C-----		
	-----Majority		
	450	460	470 480
128	-----		
141	-----		
161	-----		
	-----G P G G-----Majority		
	490	500	510 520
128	-----		
141	-----G P G G-----		
161	-----G P G G-----		
	-----P X X K X K X K X-----Majority		
	530	540	550 560
128	-----C A S-----		
145	-----C A S-----		
161	-----C A S-----		
	-----Majority		
	570	580	590 600
131	-----P-----		
153	-----P-----		
161	-----P-----		
	-----X W X-----Majority		
	610	620	630 640
112	-----T W P-----		
153	-----T W P-----		
161	-----T W P-----		

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-----XKPKKKY-----				Majority
	650	660	670	680
133	-----SSPSMAW-----			CARD4-Y CLONE
133	-----SSPSMAW-----			CARD4-Z CLONE
641	ISFNQVQAMPTFTWMLRCITETQSQKVGQLAARGICANYL			CARD4L
-----XCKXX-----				Majority
	690	700	710	720
142	-----TSCTRT-----			CARD4-Y CLONE
133	-----TSCTRT-----			CARD4-Z CLONE
651	ALTVCNACGSADCSALSFVLHHPKRLALDLDNNNLNDYGV			CARD4L
-----				Majority
	730	740	750	760
148	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
711	FELQPCFSRLTVLRLSVNQITDGGVXVLSSELTXYKIIVTY			CARD4L
-----ECK-----				Majority
	770	780	790	800
148	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
761	LGLYNNQITDVGARYNTKILD ECKGLTHLSLYNNQITDVG			CARD4L
-----WXXXXXXXXXX-----				Majority
	810	820	830	840
148	-----			CARD4-Y CLONE
133	-----			CARD4-Z CLONE
801	ARLGKNKITSEGGKYLALAVKNSKKSISEVGMWGNQVGDEG			CARD4L
XXXXXXXXLXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX				Majority
	850	860	870	880
149	-----			CARD4-Y CLONE
133	-----LRKQA-----			CARD4-Z CLONE
841	AKAFAEA L R N H P S L T T L S L A S N G I S T E G G K S L A R A L Q Q N T			CARD4L
XX				Majority
	890	900	910	920
149	-----			CARD4-Y CLONE
131	---QVL-----			CARD4-Z CLONE
881	SLEILLWLTQNELNDEVAESLAEMLKVNQTLKHLWLIQNQI			CARD4L
XX				Majority
	930	940	950	960
149	-----			CARD4-Y CLONE
134	-----			CARD4-Z CLONE
901	TAKSTAGLADALQSNTTETETICLNGNLKPEEAKVYEDEK			CARD4L

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<u>C X X X F</u>				Majority
149				CARD4-Y CLONE
154	- - - -	F		CARD4-Z CLONE
161	F - - -	C F		CARD4L
Decorations: Decoration #1: Shade (in solid black) residues that match the Consensus exactly.				

CCACGCGTCCGCGGACCCCGAGCGGTAGCGCCCTCCCTCCACAGCTGTTGTCCCGCCCGAT
 CCGCGACCCTAGTCCCGCGATCCCGTTGCTGAGAGTCACCGTACTCCAGGGCCAACTGAG
 CCAAAGTCCTGCCAACTTGGGTGAGCAATGAAAGGCAGGATCCTGGGTGGTGGCCCTGAA
 TCCTGATTTGTCTGCCCTGCCAGCGAGACACATGTGGTCAAAGATGAATTTGAGAAAAGT
 AGCTGCTGGCTACTTGAACAATGGAGGAACACGGCCATCATGAGATGGAAGGCACCCCAT
 TGGGTTGTCACTCCACATTAAGTCTGTAAGATCAACAGGGAACATCTGGTCACCAACA
 TTCGGAACACTCAGTGTCTGGTGGACAACCTTGCTGGAGAATGGGTACTTCTCAGCCGAAG
 ATGCAGAGATTGTGTGTGCTGTCCCAACCAAGCCTGACAAGGTCCGAAAGATCCTTGACC
 TGGTGCAGAGCAAAGGCGAGGAGGTGTCTGAGTTCTTCCTCTACGTGCTGCAGCAGCTGG
 AGGATGCTTACGTGGACCTCAGGCTGTGGCTCTCAGAAATTGGCTTCTCCCCCTCCCGAGC
 TCATTCCGACCAAAACTATCCTCAATACTGACCCAGTAAGCAGGTATACCCAACAGCTGC
 GACACCAACTGGGCGCGACTCCAAGTTCATGCTGTGCTACGCCCCAGAAGGAGGACCTGC
 TGCTGGAGGAGACCTATATGGACACACTCATGGGGCTGGTAGGCTTCAACAATGAAAACC
 TGGGCAGCCTAGGAGGCCTGATTGCTGCTGGACCACAGTACGGGCGTCTCAACGAGC
 ATGGCGAGACTGTCTTCGTGTTCGGGGACGCGGGAGTGGGCAAGTCCATGCTGCTGCAGA
 GGTTCAGAGCCTCTGGGCGTCAGGCAGGTTGACCTCCACAGCCAAATTCTTCTTCCACT
 TCCGCTGCCGATGTTTCAAGTCTCTTCAAGGAGAGCGACATGCTGAGTCTGCAGGACCTGC
 TCTTCAAGCATTTCTGCTACCCGGAGCAGGACCCCGAGGAGGTGTTCTCCTTCTTGCTGC
 GCTTTCCCCACACAGCGCTCTTCACTTTTGACGGCCTGGATGAGCTGCACTCAGACTTCG
 ACCTGAGCCGCGTGCCGGATAGCTGCTGCCCTGGGAGCCGGCTCACCTCTGGTCTGCTGC
 TGGCTAACCTCCTAAGTGGGAGGCTGCTCAAGGGTGCCGGCAAATTGCTCACTGCTGCA
 CAGGCGTGGAGGTCCCCCGCCAGCTCTGCGCAAAAAGGTGCTGCTCCGGGGCTTCTCCC
 CAAGTCACCTGCGCGCCTATGCCCGCCCGATGTTCCCCGAGCGCACAGCGCAGGAGCATC
 TGCTGCAGCAGCTGGATGCCAACCCCAACCTCTGCAGCCTGTGCGGGGTGCCGCTCTTCT
 GTTGGATCATCTTCCGTTGTTTCCAGCACTTCCAGACGGTCTTCGAGGGCTCCTCTTCAC
 AGTTGCCCGACTGTGCTGTGACCCTGACCGATGTCTTTCTGCTGGTCACTGAGGTGCATC
 TGAACAGGCGCGAGCCAGCAGCCTGCTGCAGCGCAACACGCGCAGCCCGCGGAAACCC
 TACGTGCAGGCTGGCGCACGCTGCATGCGCTGGGAGAGGTGGCTCACCGAGGCACCGACA
 AGAGCCTCTTTGTGTTTGGCCAGGAGGAGGTGCAGGCGTCCAAGCTGCAGGAAGGAGATC
 TGCAGCTGGGCTTCTGCGGGCTTTGCCCGATGTGGGCCCTGAGCAGGGCCAGTCTTACG
 AATTTTCCACCTTACGCTCCAGGCCTTCTTCAACCGCTTCTTCTGCTAGCAGATGACA
 AAGTCAGCACCCGGGAGTTGCTGAGGTTCTTTGAGAATGGACGTCTCCTGGAGAGGCAA

FIG. 15 (Page 1 of 3)

[illegible]

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CTCCACAGCAGCAGGCGATGGCTTGCCTCAATGGTCCCTCAGATCCCAACAAAACCTCTCTCC
CTTGCCTGTGAGCAGAAAGTATCTTCATGTCTCCTCAGAAGTTGGAGGGTGCCTGACACAG
TTAAGACTCAGAGAGCCAGCTGATAGCTCAAAGCAAAGCATGGCCACATACCCACCACCAT
ACCATGGTGGCGCATGGGATGGGACAGTTGGAATGTTGCAGATAACGTGTTCTTTTGGCCAG
TTCATTGTGTTAATAAAATATTTTAAACGTTAAAAAAAAAAAAAAAAAAAAAAAAAGGGCG
G (SEQ ID NO:42)

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	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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MEERHGHHEMEGTPLGCHSHIKLLKINREHLVTNIRNTQCLVDNLLNGYFSAEDAETVCA
OPTKPKVRKILDLVQSKGZEVSEFFL77LQQLEDAVVDLRNLSEIGFSPSOLIRTKTI
VNTDPVSRYTQQLRHQLGRDSKFMCLYAQKEDLLLEETVMDTLMGLVGFNNENLGSLLGGL
DCLLDHSTGVINEHGETV7FVFGDAGVGKSMLLQRLQSLWASGRILTSTAKFFFFHFRCRMFS
CFKESDMLSLODLLF7GHFCYPEQDPEEVFSFLLRFPHTALFTFDGLDELHSDFDLSRVPD
SCCPWEPAHPLVLLANLLSGRLLKGGKLLTARTGVEVPRQLLRKKVLLRGFSFPHLRAY
ARRMFPERTAQEHLLQQLDANPNLCSLCGVPLFCWIIIFRCFQHFQTVFEGSSSQLPDCAV
TLTDVFLLVTEVHLNRPOFSSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLFVFG
QEEVQASKLQEGDLQLGFLRALPDVGPEQGQSYEFFHLLTQAFFTAFFLVADDKVSTREL
LRFFREWTSFGEATSSSSCHSSFFSFQCLGGRSRLGPDPPFNKDHQFQFTNLFVCGLLAKAR
QKLLRQLVPKAILRRKRKALWAHLFASLSYLKSLPRVQSGGFNQVHAMPTFLWMLRCIY
ETQSQKVGRLAARGISADYKLAF7CNAC7SADCSALS7VLHHFHRQLALDLENNNNLNDYGV
QELQPCFSRLTVIRLSVNOITDTGVKVLCEELTKYKIVTFLGL7NNQITDIGARYVAQIL
DECRGLKHLKLGK7NRITSEGGK7VALAVKNSTSIVDVGMWGNQIGDEGAKAF7EALKDHP
SLTTL7SLAFNGISPEGGKSLAQALKQNTTTLTVIWLTKNELNDESAECFAEMLRVNQTLRH
LWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRIICF
(SEQ ID NO:43)

FIG. 16

Variable	Mean	SD	Min	Max	Median	Q1	Q3	Mode	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.2	12.5	18	65	32	28	38	35	0.15	2.1	0.98	Normal
Gender	1.2	0.4	1	2	1	1	1	1	0.05	0.2	0.99	Normal
Marital Status	2.1	0.8	1	3	2	1	3	2	0.12	1.8	0.97	Normal
Education	15.8	2.5	10	20	16	15	17	16	0.08	0.5	0.99	Normal
Income	1250	350	500	2500	1100	800	1400	1000	0.25	1.5	0.95	Normal
Occupation	1.8	0.6	1	3	2	1	3	2	0.10	1.2	0.98	Normal
Health Status	2.5	0.5	1	3	2	2	2	2	0.02	0.1	0.99	Normal
Stress Level	3.2	1.0	1	5	3	2	4	3	0.18	2.5	0.96	Normal
Life Satisfaction	4.1	0.8	2	5	4	3	5	4	0.05	0.3	0.99	Normal
Resilience	3.8	0.9	2	5	4	3	5	4	0.08	0.6	0.99	Normal
Optimism	4.3	0.7	3	5	4	4	5	4	0.03	0.2	0.99	Normal
Emotional Stability	3.5	0.6	2	4	3	3	4	3	0.04	0.4	0.99	Normal
Self-Esteem	4.0	0.7	3	5	4	3	5	4	0.06	0.5	0.99	Normal
Life Satisfaction	4.1	0.8	2	5	4	3	5	4	0.05	0.3	0.99	Normal
Resilience	3.8	0.9	2	5	4	3	5	4	0.08	0.6	0.99	Normal
Optimism	4.3	0.7	3	5	4	4	5	4	0.03	0.2	0.99	Normal
Emotional Stability	3.5	0.6	2	4	3	3	4	3	0.04	0.4	0.99	Normal
Self-Esteem	4.0	0.7	3	5	4	3	5	4	0.06	0.5	0.99	Normal

FIGURE 17

[illegible]

FIG. 18 (1 of 10)

[illegible]

FIG. 18 (2 of 10)

ctgtcacaccagtggtcagagtgtaaataattgcatggggacatgggggtgcaggggggtcgaaggct
 gccctagcctgggaattggaaaacctggagtctgttctctgtactctcagccagtgactctccct
 ctgtagccccaggcagtcctcacactcagtgccacctctgtccatctttttttttctccccaa
 atggaggtcccgtctgttggccagggtggagtgagtgagggtgatctcagctcactgcaacctcc
 gcctcctgggttcaagcgattctcttggccagcctcctgagtagctgggattacagggcacacgc
 caccatgtccggctaagttttttgtatttttagtaggacgggggtttccccatgttggccaggctg
 gtcttgaaatcctgacctcaggtgatccgcccgcctcggccttccaaaatgttgggggttacaggc
 atgagccgcgcacccgacccctctgtccatcttttcaatgggaaactccacaccagtggtggtg
 ccctgcccttctgtgtccccagggtgaagcttccctcacaccagtgcaagaaaaaacagcttg
 taggaaagcagaggatattgggtaaccacgggaagcacactcagttctctgggtgcatcagttagg
 attagtttttagctgagagcgaaaaacccccaaatgttgggtgagttacaagcttatttctctcatgta
 aaagtctagaggtaggtagttcaggactggtagtgaggtcctcagctccggagctccggagcactc
 tcttctgccttctgttctgtccatcctcactaccggcttccccatcttggcccaagaggggtgc
 tcaaaactccagccatctagtgcacactctagctatcagtaagaaggaagggcaagattgagagc
 atgcctcaatcttttaagaacacttcttgggtattactaattatattgctgcttagatttcagaa
 cttaatgggtatgggcagaatttaatagagatgggcccagctaaaagatgggggaatctattgctaa
 gaaagtatagatattgggaatgtctagcagcctgtgctgtcttgggtggccatgccatgtacat
 acacactatttcccagcaccaagctggggactctgagggaaaagggccagagtgctgacttgat
 catcttgatgtggcctaaaaatcaagcttttaattgttcagcctttacttggtatcaaggtcag
 cttgtgggtctaattggggcccaaggcttgtgtttctaaagtaaagttttattggaacgcagccata
 cccattttacttacttggtgcttccactacacagttgagtagctgtgacagagaccacatg
 gccacagagcctaaaaatatttgcgtgtgacactttacagaatgacatgagcagctccttttga
 cagtgaggactcacagcctttccagtgacaaaatcaggggtagcccatgtgttctggatgggggg
 aagctgttggcattttgggtataacagttcttgtgagacctgtccagcattttgaggaccccta
 acatcattggccctgcctgcaagatgacagggcactccctcctccagtcacaaacctaaaagca
 gccctgacatttccaaacctatgcctccaccatacagagaaccaggtacaggggtctgggtgaca
 catagggtcacacgcaaaggggtggatgtcagaggtgggtggcctcacacgtcctccctgtgtcctt
 cacgggtcgtgtgaggagccaggggtgtgtgtgcagcctcgtcatggggtgggtgcaggatgggtc
 tggcgggccccacgttggccaggcttgttaaggggtctatttgggtgattgctgtggccattctcca
 gggcggtctatacctgagaaaaactccagggcctgaaggcttctggatctttgttaagattaatgggt
 ccttcataatgagtgacctgcctgactcgtaattttttgtgttttatttcagactcagcgtaa
 accagatcactgacgggtgggggttaaagggtgctaagcgaagagctgaccaaatacaaaattgtgacc
 tatttgggggtatgtcttctccagaacactgggccaactacctagtaataatacagagctgcagg
 gaattcacattcccatagggtccctggatgatcgggcacggatggcccaggggtgggaagagcgctg
 gcccaggagttgagagtcctgggttctcttgtgggtcggccagtcaggaagtcttgcgtgagcct
 cagcctcctcacctgtaaaaactgggatcccagtataggcaagtaggcttacaactgggtattggg
 ggatgcaacgagaatataaggggatataatttaataatgctagaatcctgtttacataattagtcct
 ggactattttgggtccataatccctcatccagagcctttggggcaagaccggaatggggattctg
 agtgcatgctatggcatgacgtggccgaggggtctaaggcagtgccccattttcaaacactttc
 atatttctccgcgagaatgtatgaaacagtcacaaagtggtggttaagaaagactataagtagct
 ccacatcagttgccccaaagaattgtgagaaactttgggcattcagagcctttgaggttttggagt
 ctgagagaagggattgcggggccagccccacacaactgggtggctctgcaagctggagcagttgttc
 agtttcttggggcctcagtgcccttcgatgttaatgaggacatggagcgaacgacccccgggcca
 cactcgggtccagggtctgtgtgggtgtggaaccttgggaagcctgagcttagctgcctttcaac
 ttccatctgctgtactattgaattggcattgagcgggtgagatgggtgaaaggtagacatcgagaa
 gttttaatatcagaatcttttcttcaagacgctgaatgtaactcttagttgttaatacccatc
 acctgccagtcaccgagcactcatgcaccagggttttgcgttatgtcctaagatcctcataacca
 ccctgcaaggggactatcatcattacctctgtattacagatggagaaactgaggcacagagaggt
 aacgtgactgtctcaggccataaaagctggggaaagtagtgaggtgggttttgaacctgagctgt
 gagacctcagagccctaaactcgtgtgcctgtgtgttcccccttcaacccagactttggaaatca
 gtagacaccatagcttcaaaaaacaggggtctataaaatgacatcaggagccagaaagtctcat
 ggctgtgctttctcttgaagtttatacaacaaccagatcaccgatgtcggagccagggtacgtcac
 caaaatcctggatgaatgcaaagcctcacgcatcttaagtaagtggttaggcaccaggttctc
 tagtatattctcttgatcccccttctgttgttcaaagattaaatgtcacagtaaaagagcttc

FIG. 18 (3 of 10)

atcctaaagccttccacttgtcccagggccatgttgggtcaagtaagataacctctgtgtgatctg
 tgaggccttggattctggaagggcctcccgttattggtagggggaaaggttggcattttgatttca
 ttaactactaggccgaagaaaggactaactctcaccctttctgggtgggtctttttgccccaaagga
 gtttccctgtcggttgcgaaggaagagcttgggccccttgccctgctgttaggtgtgcccgtgcgcagg
 ggggtgacagtgcgccaggcttggagcctctgggtcctgcccgtgacagtggccacataacctgaccc
 ttggcagtcaaagtgggacctcccagggtctcccaggggaagtcaagtgtgtgtgtgaggtcaatt
 agaggaccccaggagggtcagggtccctgagcttctgcagagactgtggaccatctcctggaga
 ggaacctgactgactgtcctcagggcctcagttccctccctgacaggaggccaggccatgggt
 cttgtggatcccagaagaaagtgtacgggtcccaagatggggctggaaggggtctgtgtgtggg
 aggagggtgacccacattggagcccctgcatagctggagggtgactgtgtgtgactctctctgca
 gactgggaaaaaaacaaaataacaagtgaaggagggaagtatctcgccctgggtgtgaagaacagc
 aaatcaatctctgaggttgggtgagtagaaggggatggatgtatgtggtacaacctgctgtgtgt
 gtggggggcgggccttgcgttcttttcatatcagtagacaccagaaggaccatggggctcgct
 gtccgggagagatagtggagagcttccaccatgctgcgaaactgaaacctgcccattaaagcaat
 aactccccgggtccccctccccctgcctcttgcagccacctgctacttactctctctatgggtt
 tgactactctacctcatgtaagtgaatcatacagtatttgccttttggggatggctgatttcac
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 gcttaataacctcctcttgaaatctcacacaccagtggtggggggcactcttatagttattct
 cagtttacagatgacacaactgaggcacagacagatgcgtttatttcttcaaggttctgtagctg
 aacagtggggagggaggggtttagaggagctgcacccgctctgcaatactgctctcacgagggga
 gtccctcttcatgacagcatagggccctcgtcttccctggtaagggctccttcttgggtcag
 tgccaggatttctaagggtcatgtttagcaggagcctattctacaaacagccaggagcagggaaat
 gactctgtgatgaagcggagacactacagcctcttgatgcatttttccctgggtgggttagaag
 cgtagctgcccagggagcatttcaggagagggcctggcttccctagcgtatgctgaaaactttgtt
 tcatttgaatcactgctacccagaacaatgggggtgcattctcagagtccccattattaaagcttt
 tccactgagcccatgagaactattcatgagaactatttcatggcagcataactgtttctcctcc
 ctccctcttgcattgttggtagcctcttaactttaaaacctgcttgccttccctagctacctgg
 aaggagacgtcagacttccctgtcccatgggtgtgtttcttacaatttgttgggtcagattgggtggtc
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 cgatcttgggtcactgcaacctccacctccaggttcaagcaattctcctacctcagctctcccgag
 tagctgggagtagcaggtgcacaccaccatgcccagctaattttttgtatttttaataagagacag
 gttggccaggatggtatcgatctcctgagctcgtgatccacccacctcggcctcccaaagtgtctg
 ggattacaggtgtgagccactgcacccggccccaaatattttgattatgcacctctgcagtgaaa
 aatgcaaacacacacatcagttcatgtattacattatgttcactataaaaaacaaacagaaaaattt
 aaaaaatataagctatccttttactctagtggtatttacctggagacttttagccagatacaaaag
 tcacatggactcagttcttccctgaccaacttgtctcttatcccaaacaccttgaactccc
 ttacgaaggggtcaaatttgatccagttatttggttttatacaagttatgttcttcttccagggc
 ttatccagaatcagatcacagctaaggggactgcccagctggcagatgcgttacagagcaaacact
 ggcataacagagatttggtaagatcccagcgtttgtcacagtaataacaccagtgactgtttact

caccaccactgactgtgcaaggcacaacgcagggtggtttctgtttattcctccagcaaccctgc
 acagtaatggtattacctctgttttacagaggttagacagagggccagaccagtgaataaggttg
 cccaagggtcactacgagagaagctagaattcagcccagaatgcctgattccatattctgtgctct
 cctgcccctgggccccccgcccctcatctaccttcattgggtgggatgggggaagtggccagtgaat
 gatttcctagtggagtaaatccccctgggactcagcaattgagagatgactgtgttggccagga
 gtttggagctcattctccctttttctgggtccgtaagacatttcagggtgacttgaactgac
 ctgtgctctttgtctacttctttttctgtcttgagaacttcttatgctaatagaagaaaaaa
 gtttgccttactgtgacattgagcgccatgccacttctttcttgcctcccataaggcagagacac
 tccccactcagcagctcccttaacaacttaattgcctgggtgacgtgggactgggtggatgctgg
 gagaggggcccatttaactatgtcctcctttcatgactggggagaatttcataagccaattaaaaa
 aaaacaaaaaacagctccttggccaacacagggtcctcatacagtgttttttaactttgcttta
 gaacttggttggaaactgtcataaaatcgatcagtttgggtgaattgcaaccaacaatatataaaa
 agaaaaacagaacagaacaaaaatcaggtatgcattgtgcatggtatgaaagtatcatttcattca
 tcttagttcatgcttgcatgtgagtggtgtgtgtttgcataagtggttgcataacataaaaat
 gtaattcttatttaggggtttagacaaaagggttttttttaaaaaaacactgttggctaggcat
 ggtggctcatgctgtatataccagcacttggggaggccaagatgggcagatctcttgagcacagg
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 gctgcagtgagccaggatcatgccactgcaatccagcctgggtgccagagaccctgtctcaaaaa
 acaaaaaagaaaaaaagaaaaacaccatcatagagaatagagccagatctaacaacagacactgt
 ggctgtgtgctgcgaagcccagcctgccagcagcctgggaagcactggagggcactggaact
 gtttgcagtggtgtttgcccctcaggccactccgtttctgtgatttcttaagttttgaggacagca
 ggcagagggggagaggaaggagactgccagactacagaacagtttgagagcacagttggcttcc
 acttttctctgtagctggtcaggcgggtagttaaagacctacagttgctttaattctgtcaagttt
 caaaatctgcattgcttccctcttgagggtcaccatttctacacaaggaaccatttttagtagggc
 caggagacttcagcttcaaggcctgcacttgtgtcagggtggagaggggaactggccaccaattc
 agagaggggcaggacaggcggcatgggtgctggtcttgggagtgcttctacttaggtccctggctt
 gttctgggagcctccagagcatgctcctctgtgtgtgacttcatgggactgggctctgagaaggc
 tgtggctttgttggccctgccagggactgccacaccaggccacagggttgtgggtgagctggccg
 gggagccacgttcaggagcagctctgcttggagccaacacttacagagtaagccttctccttgg
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 agtcccttgatgagttctgtctttaaagaacagaaattagaggtgaacaatgaacactgtataatta
 cagaaatgtatcccactccagtataacagctttctgtgaggctatctcctccagactgtggctct
 gggagggtggggcctgagtcaaggctcctagggactagtgtgtgtcttcatatttattccttgaata
 acgaaacgcttgagcatcagggactgtgctagcaccacaaaatccagtggtgaacaacatggcttc
 atgggttactgtctagaaaggggagaagcacattaaagaaaaaatcatttgcgtaattatttaaat
 tacaactgtatgggtactatcacaaaggggaaggccaagaggggaacctgatttagatgaggttg
 cagggaaggcctctctgaggaagcagcacttacactaagccatgaaggatgaataggagctagtc
 agctgaggtgagttattctgcgtagggaacagcatgtgcaaaagggtctggggcaggagggagtggtg
 gtgtcctggaagaactgccagaagctgctgtgccccagggttcagacagtggtggaagaggggact
 acaggaggctgaggagataggcagggactggaccataaaaagatctgtgggtcatgatgtgcattt
 tggcttttatcctaaaagtgtatggaaagttagtgaacagtttgaagcaggagagggcatgtgatca
 gatctgcaatgcaaaaagaccaattcttggctcttctagggaaactgaattggagaaggccagagt
 acgtggaaatgacctgtcagtaggacattgtactgatgcagggaagagatgatgggtgctcagac
 caagatggccggccaaagacatagaggttccaggggaggcattcttagaatttagggga
 gaactttgtgatacaaggaacatggggatgagaaggaagggtgtccaggttgacccccagggttact
 aacctgtcagcaggatgagagtggtccattcactaagccaggggaccctaggaggtgtggctac
 tttgaggtgtgggggagaggtccaagtgaggatgccaaagcaggtaactgcctccacggacataca
 acaaggccgtggcattgatgagatcggttggggaaaagggttagcccccacactggaggaaat
 ctcatgttagaggtcacatggaggagaatataggaaaggaatgaagttagagtgctcagatgc
 aggagaaaaatcagcgcatataaccaagccaagggagggtgctcaagaaggagggagagga
 gaggtcaggacagccaaaatcctgaggggccaagaaagacaagacctggaaaatgtcattaaattc
 aggttatggaggctacaggtgaccttagtgagacccagtgaaacagagggatggcagctggagag
 gatccatgctaataatgaaggaactatctgcaaaagggtatgttcccttaatttcagggatacatgtg

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tattgtgtgatacacgagtgtgtgctatgaacacaccttgggaaggagtgtgagaggatccttaa
cattttacctgtgtacttttgtcttccctcttttcaacagcctaataatggaaacctgataaaacca
gaggaggccaaagtctatgaagatgagaagcggattatctgtttctgagaggatgctttcctgtt
catgggggtttttgccctggagcctcagcagcaaatgccactctgggcagtcttttgtgtcagtgt
cttaaaggggcctgcgagggcgggactatcaggagtcctactgcctccatgatgcaagccagcttc
ctgtgcagaaggctctggtcggcaaacctccctaagtacccgctacaattctgcagaaaaagaatgt
gtcttgcgagctgtttagttacagtaaatacactgtgaagagactttattgacctattataa

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1 GTGACCCACCGCTCCGGCAGCAGGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAAGG
CAGCTGGGTGCGCAGGCCGTGCTCCGTCCGACGTGCTCCGCTCGTCTCATTTTCC

63 TGACCGCGGCTGCCCACCCAGAGCCATGGGGCGGGCAGAGATGCCATCCTGGACGCTCTT
ACTGGCGCCGACGGGTGGGGTCTCGGTACCCCGCCCGTGTCTACGGTAGGACCTGCGAGAA
----- 1 M G R A R D A I L D A L -----
125 GAAAACTTGTTCAGGGGATGAAGTCAAAAAGTTCAAGATGAAGCTGCTGACAGTCAACTGCG
CTTTTGAACAGTCCCTACTTGAAGTTTTCAGTTCTACTTCGACGACTGTTCAGTTGACGC
----- 13 E N L S G D E L K K F K M K L L T V Q L R -----
187 AGAAGGCTATGGGCGCATCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCACTG
TCTTCGATACCCGCTAGGGTGGCGCCCGGGACGACGCTACCTGCGGTATCTAGAGTGAC
----- 33 E G Y G R I P R G A L L Q M D A I D L T -----
249 ACAAACCTTGTTCAGTACTATCTGGAGTCTGATGGCTTGGAGCTCACAATGACTGTGCTTAGA
TGTTTGAACAGTTCGATGATAGACCTCAGCATAACCGAAGCTCGAGTGTACTGACACGAATCT
----- 54 D K L V S Y Y L E S Y G L E L T M T V L R -----
311 GACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAACGACTAAAGAAGAGTCTGGAGCTGT
CTGTACCCGAATGTCTCGACCGACTCGTCGACGTTTGTCTGATTTCTTCTCAGACCTCGACA
----- 75 D M G L Q E L A E Q L Q T T K E E S G A V -----
373 GGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGGACACTTTTGTGGACCAGC
CCGTGCGACGTGGTTCACAGGGACGAGTCTCATGTGCGGTCTGTCTGTGAAACACCTGGTCC
----- 95 A A A A S V P A Q S T A R T G H F V D Q -----
435 ACAGGCAAGCACTCATTGCCAGGGTCACAGAAGTGGACGGAGTGTCTGGATGCTTTGCATGGC
TGTCGGTTCGTGAGTAACGGTCCAGTGTCTTCACTGCCTCAGGACCTACGAAACGTACCG
----- 116 H R Q A L I A R V T E V D G V L D A L H G -----
497 AGTGTGCTGACTGAAGGACAGTACCAGGCAGTTGCTGCAGAGACCACCAGCCAAGACAAGAT
TCACACGACTGACTTCCCTGTCTGCTCCGTCAAGCACGTCTCTGGTGGTGGGTTCTGTTCTA
----- 137 S V L T E G Q Y Q A V R A E T T S Q D K M -----
559 GAGGAAGCTCTTCAGCTTTGTTCCATCCTGGAACCTGACCTGCAAGGACTCCCTCCTCCAGG
CTCCTTCGAGAAGTCAAAACAAGTAGGACCTTGGACTGGACGTTCTGAGGAGGAGGTCC
----- 157 R K L F S F V P S W N L T C K D S L L Q -----
621 CCTTGAAGGAAATACATCCCTACTTGGTGATGGACCTGGAGCAGAGCTGAGGTATCTTTTCC
GGAACCTTCCCTTTATGTAGGGATGAACCACTACCTGGACCTCGTCTCGACTCCATAGAAAAGG
----- 178 A L K E I H P Y L V M D L E Q S -----
683 AGCTACATTATCTAGCTCCTGACTTTGTATACACAATTTTGAACCAATTTGTATTGT
TCGATGTAATAGATCGAGGACTGAAACATATGTGTAAAAACTTTTGTAAACATAAACA

745 GTTTAAAAAAGGGCGGCGCG
CAAAATTTTTCCTCCCGCGCG

FIG. 19

1 CGCGTCGGGCTGCAGCGGGGTGAGCGGGCGCAGCGGGCGGGGATCCTGGAGCCATGGGGC
GCGCAGGCGGACGTGCGCCCACTGCGCGCGCTGCGCGGCCCTAGGACCTCGGTACCCCG
1► M G

61 GCGCGCGCGACGCCATCCTGGATGCGCTGGAGAACCTGACCGCGGAGGAGCTCAAGAAGT
CGCGCGCGCTGCGGTAGGACCTACGCGACCTCTTGGACTGGCGGCTCCTCGAGTTCTTCA
3► R A R D A I L D A L E N L T A E E L K K

121 TCAAGCTGAAGCTGCTGTGCGGTGCGCGCTGCGCGAGGGCTACGGGCGCATCCCGCGGGGCG
AGTTTCGACTTCGACGACAGCCACGGCGACGCGCTCCCGATGCGCGCTAGGGCGCCCCGC
23► F K L K L L S V P L R E G Y G R I P R G

181 CGCTGCTGTCCATGGACGCGCTTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGA
GCGACGACAGGTACCTGCGGAACCTGGAGTGGCTGTTGACCACTCGAAGATGGACCTCT
43► A L L S M D A L D L T D K L V S F Y L E

241 CCTACGGCGCGGAGCTCACCGCTAACGTGCTGCGCGACATGGGCGCTGCAGGAGATGGCGG
GGATGCCGCGGCTCGAGTGGCGATTGCACGACGCGCTGTACCCGGACGTCTCTACCGCG
63► T Y G A E L T A N V L R D M G L Q E M A

301 GGCAGCTGCAGGCGGCCACGCACCGAGGGCTCTGGAGCGCGCCAGCTGGGATCCAGGCCC
CCGTGCGACGTCCGCGGCTGCGTGGTCCCGAGACCTCGGCGCGTTCGACCCCTAGGTCCGG
83► G Q L Q A A T H Q G S G A A P A G I Q A

361 CTCCTCAGTCGGCAGCCAAGCCAGGCCTGCACTTTATAGACCAGCACCGGGCTGCGCTTA
GAGGAGTCAGCCGTGCGGTTCCGTCCGGACGTGAAATATCTGGTCTGGCCCCGACCGGAAT
103► P P Q S A A K P G L H F I D Q H R A A L

421 TCCTGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTCTGTACGGGAAGGTCTTGACGG
AGCGCTCCCACTGTTTCAACTCACCGACGACCTACGAGACATGCCCTTCCAGGACTGCC
123► I A R V T N V E W L L D A L Y G K V L T

481 ATGAGCAGTACCAGGCAGTGCAGGCGGAGCCACCAACCAAGCAAGATGCGGAAGCTCT
TACTCGTCATGGTCCGTACGCGCGGCTCGGGTGGTTGGGTTCGTTCTACGCTTTCGAGA
143► D E Q Y Q A V R A E P T N P S K M R K L

541 TCAGTTTTCACACCAGCCTGGAACCTGACCTGCAAGGACTTGCTCCTCCAGGCCCTAAGGG
AGTCAAAGTGTGGTCCGACCTTGACCTGGACGTTCTGAACGAGGAGTCCGGGATTCCTC
163► F S F T P A W N W T C K D L L L Q A L R

601 AGTCCCACTCCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTTCCAGCAACAC
TCAGGGTCAGGATGGACCACTCCTGGACCTCGCCTCGACTCCGAGGAAGGGTCTGTGTG
183► E S Q S Y L V E D L E R S

661 TCCGGTCAGCCCCTGGCAATCCACCAAAATCATCCTGAATCTGATCTTTTATACACAAT
AGGCCAGTCGGGGACCGTTAGGGTGGTTTAGTAGGACTTAGACTAGAAAAATATGTGTTA

721 ATACGAAAAGCCAGCTTGAA
TATGCTTTTCGGTCAACTT

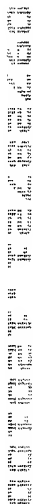


FIG. 22

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ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
 > hCARD5-DNA 740 aa vs.
 > mCARD5-DNA 763 aa
 scoring matrix: pami20.mat, gap penalties: -12/-4
 68.2% identity; Global alignment score: 2377

```

      10      20      30
inputs C---GCGTCCGGCTGCAG-CGGGGTG-----AGCG-GCGGCAGC-----GGC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      CCACGCGTCCGGCAGCAGGCTGCAGCAGGCGAGCAGCAGCAAGAGTAAAGGTGAC
      10      20      30      40      50      60

      40      50      60      70      80      90
inputs CGGGGAT-----CCTGGAGCCATGGGGCGCGCGCGACGCCATCCTGGATGCGCTGGA
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      CGCGGCTGCCCCACCCAGAGCCATGGGGCGGGCAGAGATGCCATCCTGGACGCTCTTGA
      70      80      90      100     110     120

      100     110     120     130     140     150
inputs GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGCGGTGCCGCTGCC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      AAACCTTGTCAGGGGATGAACTCAAAAAGTTCAAGATGAAGCTGCTGACAGTGCAACTGCC
      130     140     150     160     170     180

      160     170     180     190     200     210
inputs CGAGGGGTACGGGCGCATCCCGCGGGCGCGCTGCTGTCCATGGACGCCTTGGACCTCAC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      AGAAGGCTATGGGCGCATCCACGCGGGGCCCTGCTGCAGATGGACGCCATAGATCTCAC
      190     200     210     220     230     240

      220     230     240     250     260     270
inputs CGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCCGAGCTCACCCTAAC-GTGC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      TGACAAACTTGTCAGCTACTATCTGGAGTCGTATGGCTTGGAGCTCAC-AATGACTGTGC
      250     260     270     280     290

      280     290     300     310     320     330
inputs TGCGCGACATGGGCCTGCAGGAGATGGCCGGGCAGCTGCAGGCGGCCACGCACCAGGGCT
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      TTAGAGACATGGGCTTACAGGAGCTGGCTGAGCAGCTGCAAAACGACTAAAGA--AGAG-T
      300     310     320     330     340     350

      340     350     360     370     380     390
inputs CTGGAGCCCGCCAGCTGGGATCCAGGCCCCCTCCTCAGTCGGCAGCCAAGCCAGGCCTGC
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
      CTGGAGCTGTGGCAGCTGCAGCCAGTGTCCCTGCTCAGAGTACAGCCAGAACAGG---AC
      360     370     380     390     400     410

      400     410     420     430     440     450

```



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inputs ACTTTATAGACCAGCACCGGGCTGCGCTTATCGCGAGGGTCACAAACGTTGAGTGGCTGC
      .....
      ACTTTGTGGACCAGCACAGGCAAGCACTCATTGCCAGGGTCACAGAAGTGGACGGAGTGC
      420      430      440      450      460      470

      460      470      480      490      500      510
inputs TGGATGCTCTGTACGGGAAGGTCCTGACGGATGAGCAGTACCAGGCAGTGGCGGCCGAGC
      .....
      TGGATGCTTTGCATGGCAGTGTGCTGACTGAAGGACAGTACCAGGCAGTTCGTGCAGAGA
      480      490      500      510      520      530

      520      530      540      550      560      570
inputs CCACCAACCCAAGCAAGATGCGGAAGCTCTTCAGTTTCACACCAGCCTGGAACCTGGACCT
      .....
      CCACCAGCCAAGACAAGATGAGGAAGCTCTTCAGCTTTGTTCCATCCTGGAACCTGACCT
      540      550      560      570      580      590

      580      590      600      610      620      630
inputs GCAAGGACTTGCTCCTCCAGGCCCTAAGGGAGTCCCAGTCTACCTGGTGGAGGACCTGG
      .....
      GCAAGGACTCCCTCCTCCAGGCCCTGAAGGAAATACATCCCTACTTGGTGATGGACCTGG
      600      610      620      630      640      650

      640      650      660      670      680
inputs AGCGGAGCTGAGGC-TCCTTCCCAGCAACACTCCGGTC-AGCCCCCTGGCAAT-CCCAC-C
      .....
      AGCAGAGCTGAGGTATCTTTCCAGCTACATT---ATCTAGCTCCTGACTTTGTATACAC
      660      670      680      690      700      710

      690      700      710      720      730      740
inputs AAATCATCCTGAATCTGATCTTTTATACACAATATACGAAAAGCCAGCTTGAA
      .....
      AATTTTGA AAAACAATT-TGTATTTGTGTTTAAAAAAAAAAAAAAAAAAGG
      720      730      740      750      760

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ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
 > hCARD5-protein 195 aa vs.
 > mCARD5-protein 193 aa
 scoring matrix: paml20.mat, gap penalties: -12/-4
 71.8% identity; Global alignment score: 712

```

      10      20      30      40      50      60
inputs MGRARDAILDALENLTAEELKKFKLLSVPLREGYGRIPRGALLSMDALDLTDKLVSFY
      .....
      MGRARDAILDALENLSGDELKKFKMKLLTVQLREGYGRIPRGALLQMDAIDLTDKLVSY
      10      20      30      40      50      60

      70      80      90      100     110     120
inputs LETYGAELTANVLRDMGLQEMAGQLQAATHQGSGAAPAGIQAPPQSAAKPGLHFIDQHRA
      .....
      LESYGLELTMTVLRDMGLQELAEQLQT-TKEESGAVAAAASVPAQSTARTG-HFVDQHRQ
      70      80      90      100     110

      130     140     150     160     170     180
inputs ALIARVTNVEWLLDALYGKVLTDQYQAVRAEPTNPSKMRKLSFTPAWNWTCKDLLLQA
      .....
      ALIARVTEVDGVLDALHGSVLTEGQYQAVRAETTSQDKMRKLSFVPSWNLTCCKDSLLQA
      120     130     140     150     160     170

      190
inputs LRESQSYLVEDLERS
      .....
      LKEIHPYLVMDLEQS
      180     190

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1 CCCGCGTCCGGACTTCCCTTCCAGTGTGTTGTTTCTCTCTGCTCTCTCCAACAGAAGGTATTTTTG
GGGCGCAGGCCTGAAGGGAAGGTACAAACAAGGAGAGACGAGAGAGGTTGTCTTCCATAAAAAAC

66 GCATGTTTTATCTTTGCTAAGTAGGATTCTGTCTTTCTTTGTTAACACAGATTCTTTCTGTGC
CGTACAAAATAGAAACGATTTCCTTAAAGACAGAAAGAAACAATTGTGTCTAAAGAAAGACACG

131 CAGAATGACCTGATCCATTTCTGGTTTGTAGAAAGCCATGGCTTCAGAGGGTCTTCCCTCAGAA
GTCTTACTGGACTAGGTAAAGGACCAACATCTTTTCGGTACCGAAGTCTCCACGAAGGAGTCTT
----- 1▶ M A S E G A S S E -----

196 ATCATAGAAAAACAGCGAACAAAGTTGCTCAGTGTCTCCAACAAGATCCCGACTCTATCTTGGA
TAGTATCTTTTGTGCTGCTTTTCAACGAGTACAGGAGGTTGTTCTAGGGCTGAGATAGAACCT
10▶ I I E K Q R T K L L S V L Q Q D P D S I L D

261 CACGTTAACCTCTCGGAGACTGATTTCTGAGGAGGAGTATGAGACTCTAGAGGCAATTACAGATC
GTGCAATTGGAGAGCCTCTGACTAAAGACTCCTCCTCATACTCTGAGATCTCCGTTAATGTCTAG
31▶ T L T S R R L I S E E E Y E T L E A I T D

326 CTCTGAAGAAAAGCCGGAAGCTGTTAATTTTGATCCAGAAGAAGGGAGAGGACAGCTGTGTTGT
GAGACTTCTTTTCGGCCTTCGACAATTAAACTAGGTCTTCTTCCCTCTCCTGTGACAAACA
53▶ P L K K S R K L L I L I Q K K G E D S C C C

391 TTCCTCAAGTGTCTGTCTAATGCCTTTCCACAGTCAGCTTCCACCTTGGGTTTAAAGCAGGAAGT
AAGGAGTTTCACAGACAGATTACGGAAAGGTGTCTAGTCTGAAGGTGGAACCCAAATTTCTGCTCTCA
75▶ F L K C L S N A F P Q S A S T L G L K Q E V

456 TCCACGCGAGGGGACTGGAGAGGTTGTGAGGTGAGCAGGGGTTTGAAGATCCCTTTTCTCTTG
AGGTGCGCTCCCTGACCTCTCCAACAGCTCCACTCGTCCCCAAACCTTCTAGGGAAAAGAGAAC
96▶ P R Q G T G E V V E V S R G L E D P F S L

521 GGACCATAACCCAGAAATAGCAGAGCTCTCAGAAGAGAAAGAATGCCCGGGTCTGGGAGCTCCG
CCTGGTATTGGGGTCTTTATCTCTCGAGAGTCTTCTCTTTCTTACGGGCCCAGACCTCTGAGGC
118▶ G T I T P E I A E L S E E K E C P G L G A P

586 GAGTTCTTCACTGCAAGGAAAGCAGCCACAGGGAACCGGAAGTACCTTCTTGGGAGAATCAGGA
CTCAAGAAGTGGACGTTCTTTCGTGCGTGTCCCTTGGCTTTCATGGAAGAACCCTCTTAGTCCT
140▶ E F F T C K E S S H R E P E V P S W E N Q E

651 AGGGCGTGGTGCACAGCAAGTCACCGCTCCGCGTTCAGTCAAAGGAGTTGAGTATGAAGTTCCAG
TCCCGCACCAAGTGTGCTTTCAGTGGCGAGGCGCAAGTCAGTTTCTCAACTCATACTCAAGGTC
161▶ G R G A Q Q V T A P R S V K G V E Y E V P

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716 CAAGTATCTCCCTCTTAAGCGACGGGCAGAGATACGAGGAGCCAGATGATTGCTGTACTTAGAA
GTTTCATAGAGGGAGAATTGCGTGCCCGTCTCTATGCTCCTCGGTCTACTAAGCGACATGAATCTT
183▶ A S I S L L S D G Q R Y E E P D D S L Y L E
781 GAAGGGGAAGGTGAAGAGTCTCTTGGGTACCCCTGAAGATGTTTGGAGGAAGGGGCCGGCGATGA
CTTCCCTTCCACTTCTCAGAGAACCCATGGGACTTCTACAAAACCTCCTTCCCGGGCCGCTACT
205▶ E G E G E E S L G Y P E D V L E E G A G D D
846 CCCACAGTGTCTTGTATATGATAGTGAGGAGGAATGCCAGTATGAGGAAAACATGGGCTCCTCCG
GGGTGTCACGAAACATATACTATCACTCCTCCTTACGCTCATACTCCTTTTGTACCCGAGGAGGC
226▶ P Q C F V Y D S E E E C E Y E E N M G S S
911 GTGAAGACAGTAGCTGCGACGACACTTCAGAGACCTGCGTTCCATTGGAAGGGGAGAAAAGCGCT
CACTTCTGTCAATCGACGCTGCTGTGAAGTCTCTGGACGCAAGGTAACCTTCCCTCTTTTCGCGA
248▶ G E D S S C D D T S E T C V P L E G E K S A
976 GAAGAAAGAAAAAGAGTGTCTTCAACACGTCCTGTCTGTGTAACATGGATAGAAACAGAAAGCT
CTTCTTTTCTTTTCTCACAAGTTGTGCAGGACAGGACAAACTTGTACCTATCTTTGTCTTTTCGA
270▶ E E R K R V F Q H V L S C L N M D R N R K L
1041 TCTCCAGAGTTTCGTGAGGCAGTTTTCATAGACCGAGGATGTGAGTGGACACCCAAGACCCAG
AGAGGGTCTCAAGCACTCCGTCAAAAGGTATCTGGCTCCTACACTCACCTGTGGGTTCTGGGGTC
291▶ L P E F V R Q F S I D R G C E W T P K T P
1106 GAGACTTAGCTTGAATTTCTTGATGAAAGTTTCAGGCTTTAGACTCGACAGCCAGAGATTCTATC
CTCTGAATCGAACCTTAAAGAACTACTTTCAAGTCCGAAATCTGAGCTGTGGTCTCTAAGATAG
313▶ G D L A W N F L M K V Q A L D S T A R D S I
1171 CTGAGGCCCCGAGGTGGCGGGTGAAGAGAATGAAGAATTGCCGGCTGGAATAGAGAAGTTAGGCAT
GACTCCGGGCTCCACCGCCCACTTCTCTTACTTCTTAACGGCCGACCTTATCTCTTCAATCCGTA
335▶ L R P E V A G E E N E E L P A G I E K L G I
1236 TGGAGACCCCCAAACCATCCATCCCCTGATGTCTCTGCGCCTGCATGCTTTGTGCAGACAGCT
ACCTCTGGGGGTTTGGTAGGTAGGGGACCTACAGGAGACGCGACGTACGAAACACGCTCTGTCTGA
356▶ G D P Q T I H P L D V L C A C M L C A D S
1301 CCTTGCAGCGTGAAGTCATGTCAAACATGTACCAATGCCAGTTTGTCTCTTCCCTGCTACTGCCA
GGAACGTCGCACTTCAGTACAGTTTGTACATGGTTACGGTCAAACGAGAAGGGGACGATGACCGT
378▶ S L Q R E V M S N M Y Q C Q F A L P L L L P
1366 GATGCTGAGAACAACAAAACCTCTTAATGGTAGGGGCCATGAAGGACTTAAAGCAGCCCTCAGC
CTACGACTCTTGTTGTGTTTGGAGAAATTACCATCCCCGGTACTTCTGAATTTTCGTGGGAGTGG
400▶ D A E N N K N L L M V G A M K D L K Q P S A

Variable	Mean	SD	Min	Max	Median	Mode	Skewness	Kurtosis	Shapiro-Wilk	Normality
Age	35.2	12.5	20	65	30	30	0.15	2.5	0.95	Normal
Gender	1.2	0.4	1	2	1	1	0.05	1.5	0.98	Normal
Marital Status	1.5	0.5	1	3	1	1	0.10	2.0	0.92	Normal
Education	12.5	2.0	9	16	12	12	0.20	3.0	0.88	Normal
Income	1500	500	500	3000	1200	1000	0.30	4.0	0.80	Normal
Occupation	1.8	0.6	1	3	1	1	0.08	1.8	0.96	Normal
Health Status	1.2	0.4	1	2	1	1	0.05	1.5	0.98	Normal
Stress Level	2.5	1.0	1	4	2	2	0.25	3.5	0.85	Normal
Life Satisfaction	3.5	1.5	1	5	3	3	0.18	2.8	0.90	Normal
Resilience	2.8	1.2	1	4	2	2	0.22	3.2	0.88	Normal
Optimism	3.2	1.4	1	5	3	3	0.16	2.6	0.92	Normal
Emotional Stability	2.0	0.8	1	3	2	2	0.12	2.2	0.94	Normal
Self-Esteem	3.0	1.0	1	4	2	2	0.20	3.0	0.88	Normal
Life Satisfaction	3.5	1.5	1	5	3	3	0.18	2.8	0.90	Normal
Resilience	2.8	1.2	1	4	2	2	0.22	3.2	0.88	Normal
Optimism	3.2	1.4	1	5	3	3	0.16	2.6	0.92	Normal
Emotional Stability	2.0	0.8	1	3	2	2	0.12	2.2	0.94	Normal
Self-Esteem	3.0	1.0	1	4	2	2	0.20	3.0	0.88	Normal

FIG. 25 (3 of 7)

2146 ACAGTTGAAGGTGAAAACCAACAACCATGTAGTCAGACCAAAAGCCCGGCTGAAAGCGGAGCTCA
 TGTCAACTTCCACTTTTGGTTGTTGGTACATCAGTCTGGTTTTCGGGCCGACTTTCGCCTCGAGT
 ... 660▶ T V E G E N Q Q P C S Q T K S P A E S G A Q

2211 GGAGCCATCAGAGAGCCAGGGGCTCAATGTGACGACAGTCAGAATGCTCCGGTTTTCATCAGA
 CCTCGGTTAGTCTCTCGGTCCCCGAGTTACACTGCTGTCTAGTCTTACGAGGCCAAAAGGTAGTCT
 ... 681▶ E P I R E P G A Q C D D S Q N A P V F H Q

2276 CTCCAGTATACATGCCCTTATCCAGCACACCCATGGGCTTTGGCCATCAAAGCTGGAGGTAACTTT
 GAGGTCATATGTACGGAATAGGTCCGTGTGGGTACCCGAAACCGGTAGTTTCGACCTCCATTTGAAA
 ... 703▶ T P V Y M P Y P A H P W A L A I K A G G N F

2341 TACCACGTTCCCTTTGAATGCCCCCTGGTTATGGGCTCCCACTTTGGATCACAGCAGAGGGCTAAG
 ATGGTCCAAGGAACTTACGGGGGACCAATACCCGAGGGTGAAACCTAGTGTCTCTCCCGATTTC
 ... 725▶ Y H V P L N A P W L W A P T L D H S R G L S

2406 TGGTCTTTTCCATTCCCATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAACTGCCACCATC
 ACCAAGAAAGGTAAGGGTACGATTTGGGTGAGTGAGATTCCGGAAGGTTTCGATTGACGGTGGTAG
 ... 746▶ G S F H S H A K P T H S K A F Q A N C H H

2471 CCCATCCCTCCCATGCTAAACCCACTCATGTGAATCCCTCTCATGCTAACCCCACTCATGTGCAG
 GGGTAGGGAGGGTACGATTTGGGTGAGTACACTTAGGGAGAGTACGATTGGGGTGAAGTACACGTC
 ... 768▶ P H P S H A K P T H V N P S H A N P T H V Q

2536 CCTTGATGCTAAACCCACTCACTCTAAGGCCTTCCAAGCTAAACCCACTCCCTCTCAGACCTCT
 GGAACGTACGATTTGGGTGAGTGAGATTCCGGAAGGTTTCGATTTGGGTGAGGGAGAGTCTGGAGA
 ... 790▶ P C M L N P L T L R P S K L N P L P L R P L

2601 TGGAGCCAAGCTAACTGCAATCATGCCCATCCCTCCCTTGCTAAACCCCTCTCATACGAATCCCTC
 ACCTCGGTTTCGATTGACGTTAGTAGCGGTAGGGAGGGAACGATTTGGGAGAGTATGCTTAGGGAG
 ... 811▶ G A K L T A I M P I P P L L N P L I R I P

2666 TGATGCTAACCCCACTCATGTGCAGCCTTCCCATGCTAAACCCGCTCATCTACAGTCTTCCCAA
 ACTACGATTGGGGTGAGTACACGTCGGAAGGGTACGATTTGGGCGAGTAGATGTCAGAAGGGTTT
 ... 833▶ L M L T P L M C S L P M L N P L I Y S L P K

2731 CAAAACCCCTCCCATCCCAATCTACTGCAGTTTCACGGCACACAAACCTCAGCAGTCCCACTCTAA
 GTTTTCGGAGGGGTAGGGTTAGATGACGTCAGTGCCGTGTGTTTGGAGTCGTACGGGTACAGATT
 ... 855▶ Q N P P H P N L L Q F T A H K P Q Q S Q S K

2796 GCCTTCTCAGCAGAGACCCAGTCAGCCTAAATCATTCAGACCAAGCCTTCACAGGCCAGGGCCT
 CGGAAGAGTCGTCTCTGGGTGAGTCGGATTTAGTAAGGTCTGGTTTCGGAAGTGTCCGTCCCGGA
 ... 876▶ P S Q Q R P S Q P K S F Q T K P S Q A R A

2861 GCCACCCAAGAGCAGGGAGACGTTAAAGAACATACTCTGGAGATCTGGGAAATAAAGTATGGGCT
CGGTGGGTTCCTCGTCCCTCTGCAATTTCTTGTATGAGACCTCTAGACCCCTTTATTTTCATACCCGA
898▶ C H P R A G R R

2926 TTGCTTAAGTATTCTTTTTCATATAGCAAGCTGAAGAAAAGTTTGTAGTGAAGACTGATAAAAGT
AACGAATTCATAAGAAAAAGTATATCGTTTCGACTTCTTTTCAAAATCACTTTCTGACTATTTTCA

2991 AGCAAAACCCAAAAAGGTATGCAAAGTCTTAAGTGCATAGCAAAGTATCCAAGTGTGGGAAATA
TCGTTTGGGTTCATACGTTTCAGAAATTCAGTATCGTTTCATAGGTTACACCCCTTTAT

3056 TGAAGCAGTTAAAAGTAGAATCTGGCTGGGCATGGTGGCACACATCTACAGGGTTTAGCATGGG
ACCTTCGTCAATTTTCATCTTAGACCGACCCGTACCACCGTGTGTAGATGTCCCAAATCGTACCC

3121 AGGGCTCTGTCTATCCCAACTCAGAGAAGCAGGCAGATCTCTGTGTGTTTGAGGCCAGTCTGGTCT
TCCCGAGACAGTAGGGTTGAGTCTCTTCGTCCGTCTAGAGACACAAAACTCCGGTCAGACCAGA

3186 ACATAACAACGACACAAGCAAGTCCTACATCAGCCATACTACAAAATGAGACCCCATCTGGGGAC
TGTATTGTTCCTGTGTTTCAGGATGTAGTCGGTATGATGTTTACTCTGGGGTAGACCCCTG

3251 AAAAGGGTTGGATCTAACATCAAACCAAAGAAATCAGTCAAGTATTCAGAAGGCATCATTAAAT
TTTTCCCAACCTAGATTGTAGTTTGGTTTCTTTAGTCAGTTTCATAAGGTCTTCCTAGTAATTAA

3316 ACACTCAGTGGGTTACCACAACCAACCACTACTCGACAATAACCCCTAAAGGAGCAAGAAGGA
TGTGAGTCACCCAATGGTGTGGTTTGGTATGAGCTGTTGATTGGGGGATTTCTCGTTCTTCCT

3381 GTTGGGTGGGTGTTAGGCTGAACATGATTGGGGAAGAACTGAAGATAGATAAGGTCAATTCGTAAT
CAACCCACCCACAATCCGACTTGTACTAACCCCTTCTTGACTTCTATCTATTCCAGTAAGCATTA

3446 ACAGGTTATGGGACTTGTCAAATCCATTAAATGCAATATTAAGAAGCAGTGGGAATCTTAAGGCT
TGTCCAATACCCGTAACAGTTTAGGTAATTTACGTTATAATTCCTTCGTACCCCTTAGAAATCCGA

3511 ACATTAAGCTCCAGTGAGTCGCAACCCCTCCCTATTAGATGATGTGAGATTTGAACCCCACTGAA
TGTAATTCGAGGTCACCTCAGCGTTGGGAGGGGATAATCTACTACACTCTAAACTTGGGGTCACTT

3576 TGGGGTGTGTCTGATAGCCCGTGTGTGTGACAACTGTGTAATTATAAAGTGTGAAAACGTGGG
ACCCACACAGACTATCGGGCACACACTGTTTGACACATTAATATTTCACTACTTTTGACCC

3641 AGTTCAGCTTATCTGTGTGAAGAAAGGCTGCTTCAGAGGTGCCTTGGTTTTGGGTTTATGATCA
TCAAGTCCAATAGACACAACCTCTTTCCGACGAAGTCTCCACGGAACCAAAACCAATACTAGT

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3706 GCCACTGAGCAGATACTCTGCACCATTTGGTACAGTTAAATCAGCTTGCCTTCGGTAATAGCCCCA
CGGTGACTCGTCTATGAGACGTGGTAACCATGTCAATTTAGTCGAACGAAGACCATTATCGGGGT

3771 ATCTACCACATTTATCCCTTACAGGCGGAAATTAATGAATGATCAGCAAAACATCCAATTTTACCT
TAGATGGTGTAAATAGGGAATGTCCGCCCTTTATTACTTAGTCGTTTTGTAGGTTAAATGGA

3836 TAACCTTGGTACTGATTTGTATATGTATCATTCTTTATATAATAGCTAAGAAAAATTTAGCTCATT
ATTGGAACCATGACTAAACATATACATAGTAAGAAATATATTATCGATTCTTTTAAATCGAGTAA

3901 AGGGGTTCTGATATATTAGTTTAAATGGTTTGAAGTCAGAAATGTGTTAGTTTTTAAATTTAGAGT
TCCCCAAGACTATATAATCAAATTACCAAACCTTCAGTCTTTACACAATCAAAAATTTAAATCTCA

3966 TAATTGAAAAATATTGAGATGAATTTACAAAGGCTATAAGTAATGTTTTCAGAGGGTTATAATTTTT
ATTAACCTTTTATAACTCTACTTAAATGTTTCCGATATTCAATTACAAACTCTCCAATATTAAAAA

4031 GTAGACTCATACTGTTCTGAACATTTGGATAGCTTCTCGTAGTTAGCAGTGTATAGAAGAATAT
CATCTGAGTATGACAAGACTTGTAAACCTATCGAAGAGCATCAATCGTCACAATATCTTCTTATA

4096 ATTTGATTTCAGGTATTTAACCAGAGCTGCTCTTAGTTTTTAAAGTGTACCAAGAGTCAATAAAAG
TAAACTAAGTCCATAAATGGTCTCGACGAGAATCAAAAATTCACAGTGGTTCTCAGTTATTTTT

4161 GCTACATTTATCTGAACATGTGGGAACACAACCTGTGACCTTACACTTAAGAGACTGAGGAAGGGAA
CGATGTAATAGACTTGTACACCCCTGTGTTGACACTGGAATGTGAATTTCTCTGACTCCTTCCCTT

4226 ATCAAGGTTCAAGCCAGCAGCATAGTGAGACCAGGTCTCAAGACAAAACTATCCACCTTA
TAGTTCCAAGTTCGGTCTGCTGTATCACTCTGGTCCAGAGTTCTGTGTTTTTGATAGGTGGAAT

4291 AGGAAGATTTTAAAAATTTGCCTCATTAAAGAAATAAGTAAGATTTATAAATTTGACTAAATGTCA
TCCCTCTAAAAATTTTAAACGGAGTAATTCCTTTATTTTCATTCTAAATATTTAACCTGATTTACAGT

4356 CATCTTTGAACCTATGACTGTTTAAATTTTTGACTTAAAGTTTAAATTTTATTATTGTATGCGTGT
GTAGAACTTTGAATACTGACAAATTAaaaaactgaatttcaaattaaaaataataacatcgcaca

4421 GTTGTATGTGTGTCACATGTGTCCACTGCATGTATGTGGAGGCCATCAGACAATGTTGTAGAG
CAACATACACACACGTGTACACACGGTGACGTACATACACCTCCGGTAGTCTGTTACAACATCTC

4486 TCTGTTCTTTTCTCTTAGCCCTATGTGTTTTACCCACTGAGCTAGGCCACCTACTCCTATAAGTC
AGACAAGAAAGGAGAATCGGGATACAAAAATGGGTGACTCGATCCGGTGGATGAGGATATTGAG

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4551 TAATTTTAAATAGTAAATAGTTCTAAGAAGTCAATCAGGGAAAAAATGGCTGTCAAAGTCTCA
ATTAAAAATTATCATTTTATCAAGATTCTTCAGTTAGTCCCTTTTTTTACCGACAGTTTCAGAGT

4616 AAGAAAAATCGTATTAGCCATGGATAGAGACTCACCTCTTGAATCATTTGTGTCTGAGAATAGCC
TTCTTTTTTAGCATAAATCGGTACCTATCTCTGAGTGGAGAACTTAGTAAACACAGACTCTTTATCGG

4681 TAATATCACAATAATGTGTTTGTACATGTGTAGTTAATATTGTTTTTCAGAGTATTTAATCTCTC
ATTATAGTGTATTACACAAACATGTACACAATCAATTATAACAAAAGTCTCATAAATTAGACAG

4746 ATGATTATTGTAAAGATGAAAAAGAAATAGTGGCAATGTATGTGAGTATTTAATTTTGCCTGA
TACTAATAACATTTCTACTTTTTTCTTTATCACCCGTTACATACACTCATAAATTAAAACGGACT

4811 CAATTCTGTCTTTTAGAATGATAAATGTAAGAAGTAAAAATAAACGGTTTCATTCTCAGAACAACT
GTTAAGACAGAAAACTTACTATTTACATTCTTCATTTTATTTTCCCAAGTAAGAGTCTTGTTC

4876 AAGCCAGCTCACTTAAGTCTGGGCCCTGCTGGCATTGGCTAGTCTAGCTACCCCCACCCAAACAC
TTCCGGTCGAGTGAATTTCAGACCCGGGACGACCGTAACCGATCAGATCGATGGGGGTGGGTTTGTG

4941 AAAAGTTTAGAGAAGAAAAAGACTGAGTCAAGCTTGCCTAATGACTTTTGGACATAAAGTTTATG
TTTTCAAATCTCTTCTTTTACTGACTCAGTTCCGAACGGATTACTGAAAACCTGTATTTCAAATAC

5006 GTCCTAGAAAGCCTTAAAAAAGTAGGATATAAAACATGTAAATTAACCCACACATTATGTGGGT
CAGGATCTTTTCGGAAATTTATTTCATCCTATATTTTGTACATTTAATTGGGTGTGTAATACACCCA

5071 TGAGAAGCAGAAAAATGTCAGTAGAACACTCGGCCAGTGCATAAAGAAGGAAGAGACCTCTGTTT
ACTCTTCGTCTTTTTTACAGTCATCTTGTGAGCCGGTCACGTATTTCTTCCCTTCTCTGGAGACAAG

5136 TGGGTTATAAAACTGCTCTTTGTGCTCAATTGTCCCTGCTTTTGTGTTGCCAGAATGTACAAGA
ACCCAATATTTTGACGAGAAACACGAGTTAAACAGGGGACGAAAAACAAACGGTCTTACATGTTCT

5201 TTATAAAATAAACTCACTTTTACTTTTAAAAAAGGGCGG
AATATTTTATTTGAGTGAAATGAAATTTTTTTTTTTTTTTTTTCCCCC

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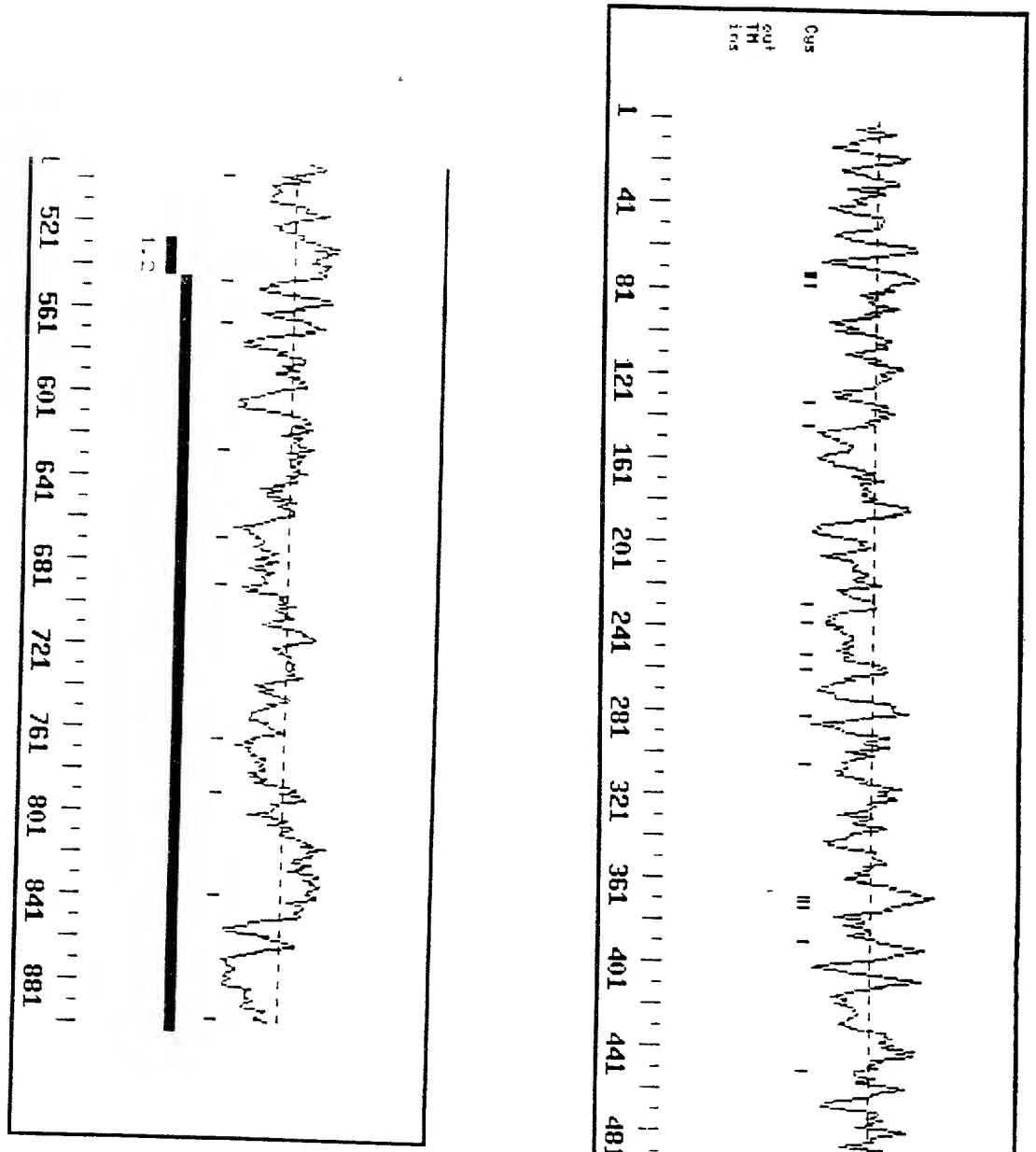


FIG. 26

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	- - - -	G X H F X D Q H R X A L I A R V T X V X X V L D A L Y - G X V L T E X Q	Majority
		10 20 30 40	
1		M E A R D K Q V L R S L R L E L G A E V L V E G L V L Q Y L Y Q E G I L T E N H	RAIDD
1	- - - -	G L H F I D Q H R A A L I A R V T N V E W L L D A L Y - G K V L T D E Q	hCARD5
1	- - - -	G - H F V D O H R Q A L I A R V T E V D G V L D A L H - G S V L T E G Q	mCARD5
		Y Q A V R A E T T X X X K M R K L F S F X P S W N X T C K D X L L Q A L X E X X	Majority
		50 60 70 80	
41		I Q E I N A Q T T G L R K T M L L L D I L P S R G P K A F D T F L D S L Q E F -	RAIDD
36		Y Q A V R A E P T N P S K M R K L F S F T P A W N W T C K D L L L Q A L R E S Q	hCARD5
35		Y Q A V R A E T T S Q D K M R K L F S F V P S W N L T C K D S L L Q A L K E I H	mCARD5
		P Y L V E D L E X S - - - - -	Majority
		90	
80		P W V R E K L K K A R E E A M	RAIDD
76		S Y L V E D L E R S	hCARD5
75		P Y L V M D L E Q S	mCARD5

FIG 27

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CACGCGTCCGCCGATCAGAGAGTGCTCCGAGCTGGGTTGCCCACTGTGCTTGTATCTGCACTCTCCAACACTAGGC 79
 ATCATTGACATGTTAAAGCTTAGCCAAATAGAATTGTCTTTGTCACTCTTTTTTAACTTTTACTTATTCATTAGGAT 158
 M A T E S T P S E 9
 GATTTTATAATATATTTCTCGTTTAGAGGAAACAGGAACA ATG GCT ACC GAG AGT ACT CCC TCA GAG 226
 I I E R E R K K L L E I L Q H D P D S I 29
 ATC ATA GAA AGA GAA AGA AAA AAG TTG CTT GAA ATC CTT CAA CAT GAT CCT GAT TCT ATC 286
 L D T L T S R R L I S E E E Y E T L E N 49
 TTA GAC ACG TTA ACT TCT CGG AGG CTG ATT TCT GAG GAA GAG TAT GAG ACT CTG GAG AAT 346
 V T D L L K K S R K L L I L V Q K K G E 69
 GTT ACA GAT CTC CTG AAG AAA AGT CGG AAG CTG TTA ATT TTG GTA CAG AAA AAG GGA GAG 406
 A T C Q H F L K C L F S T F P Q L A A I 89
 GCG ACC TGT CAG CAT TTT CTC AAG TGT TTA TTT AGT ACT TTT CCA CAG TTA GCT GCC ATT 466
 C G L R H E V L K H E N T V P P Q S M G 109
 TGC GGC TTA AGG CAT GAA GTT TTA AAA CAT GAG AAT ACA GTA CCT CCT CAA TCT ATG GGG 526
 A S S N S E D A F S P G I K Q P E A P E 129
 GCA AGC AGT AAT TCA GAA GAT GCT TTT TCT CCT GGA ATA AAA CAG CCT GAA GCC CCT GAG 586
 I T V F F S E K E H L D L E T S E F F R 149
 ATC ACA GTG TTC TTC AGT GAG AAG GAA CAC TTG GAT TTG GAA ACC TCT GAG TTT TTC AGG 646
 D K K T S Y R E T A L S A R K N E K E Y 169
 GAC AAG AAA ACT AGT TAT AGG GAA ACA GCT TTG TCT GCC AGG AAG AAT GAG AAG GAA TAT 706
 D T P E V T L S Y S V E K V G C E V P A 189
 GAC ACA CCA GAA GTC ACA TTA TCA TAT TCA GTT GAG AAA GTT GGA TGT GAA GTT CCA GCA 766
 T I T Y I K D G Q R Y E E L D D S L Y L 209
 ACT ATT ACA TAT ATA AAA GAT GGA CAG AGA TAT GAG GAG CTA GAT GAT TCT TTA TAC TTA 826
 G K E E Y L G S V D T P E D A E A T V E 229
 GGA AAA GAG GAA TAT CTA GGA TCT GTT GAC ACC CCT GAA GAT GCA GAA GCC ACT GTG GAA 886
 E E V Y D D P E H V G Y D G E E D F E N 249
 GAG GAG GTT TAT GAT GAC CCA GAG CAC GTT GGA TAT GAT GGT GAA GAG GAC TTC GAG AAT 946
 S E T T E F S G E E P S Y E G S E T S L 269
 TCA GAA ACC ACA GAG TTC TCT GGT GAA GAA CCA AGT TAT GAG GGA TCA GAA ACC AGC CTT 1006
 S L E E E Q E K S I E E R K K V F K D V 289
 TCA TTG GAG GAG GAA CAG GAG AAA AGT ATA GAA GAA AGA AAA AAG GTG TTT AAA GAT GTC 1066
 L L C L N M D R S R K V L P D F V K Q F 309
 CTG TTA TGT TTG AAC ATG GAT AGA AGC AGA AAG GTT CTG CCA GAT TTT GTT AAA CAA TTC 1126
 S L D R G C K W T P E S P G D L A W N F 329
 TCC TTA GAT CGA GGA TGT AAG TGG ACC CCT GAG AGT CCA GGA GAC TTA GCC TGG AAT TTC 1186
 L M K V Q A R D V T A R D S I L S H K V 349
 CTG ATG AAA GTT CAA GCA CGA GAT GTG ACG GCT AGG GAT TCA ATC CTC AGT CAC AAG GTT 1246
 L D E D S K E D L L A G V E N L E I R D 369
 CTG GAT GAA GAT AGC AAG GAG GAT TTG CTG GCT GGA GTG GAG AAT TTG GAA ATT CGA GAC 1306

Fig. 2B (1 of 4)

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I Q T I N P L D V L C A T M L C S D S S 389
ATA CAA ACC ATT AAT CCC CTT GAC GTG CTT TGT GCC ACC ATG CTG TGT TCA GAT AGC TCT 1366

L Q R Q V M S N M Y Q C Q F A L P L L L 409
TTG CAA CGC CAA GTC ATG TCA AAC ATG TAT CAG TGC CAG TTT GCT CTT CCC CTG CTA CTG 1426

P D A E N N K S I L M L G A M K D I V K 429
CCA GAT GCA GAA AAC AAC AAA AGC ATC TTA ATG CTG GGG GCC ATG AAA GAC ATT GTG AAG 1486

K Q S T Q F S G G P T E D T E K F L T L 449
AAG CAG TCA ACA CAG TTT TCA GGG GGG CCT ACA GAG GAT ACA GAA AAG TTT CTG ACT CTC 1546

M K M P V I S F V R L G Y C S F S K S R 469
ATG AAG ATG CCT GTC ATC TCT TTT GTG CGT CTA GGA TAC TGT AGC TTC TCT AAG TCC AGA 1606

I L N T L L S P A Q L K L H K I F L H Q 489
ATC CTC AAC ACA CTT CTC AGC CCT GCC CAG TTG AAA TTA CAC AAA ATC TTT CTT CAT CAA 1666

D L P L L V L P R Q I S D G L V E I T W 509
GAT TTG CCT CTT TTG GTG CTT CCC CGG CAA ATC TCT GAT GGC CTG GTT GAG ATA ACA TGG 1726

C F P D S D D R K E N P F F Q K P V A L 529
TGT TTT CCT GAT AGC GAT GAT AGA AAG GAA AAC CCC TTT TTC CAA AAG CCT GTT GCT CTG 1786

A N L R G N L E S F W T Q F G F L M E V 549
GCT AAT CTC CGT GGA AAT CTA GAA AGT TTT TGG ACT CAG TTT GGT TTT TTG ATG GAA GTT 1846

S S A V F F F T D C L G E K E W D L L M 569
TCT TCA GCT GTG TTT TTT TTC ACT GAC TGT TTA GGT GAG AAG GAA TGG GAC TTG CTA ATG 1906

F L G E A A I E R C Y F V L S S Q A R E 589
TTT TTA GGA GAG GCT GCC ATT GAA AGA TGC TAC TTT GTT CTC AGT TCC CAA GCC AGG GAG 1966

S E E A Q I F Q R I L N L K P A Q L L F 609
AGT GAA GAG GCT CAA ATT TTT CAG AGG ATA CTG AAC TTG AAG CCA GCA CAG CTA CTG TTT 2026

W E R G D A G D R R K N M E G L Q A A L 629
TGG GAG AGG GGA GAT GCT GGG GAT AGA AGG AAG AAC ATG GAG GGC CTT CAA GCT GCC CTC 2086

Q E V M F S S C L R C V S V E D M A A L 649
CAG GAA GTG ATG TTC TCT TCT TGC CTC AGA TGT GTG TCT GTG GAG GAT ATG GCC GCC CTG 2146

A R E L G I Q V D E D F E N T Q R I Q V 669
GCC AGG GAG CTG GGG ATT CAG GTA GAT GAA GAC TTT GAA AAC ACT CAG AGA ATT CAA GTT 2206

S S G E N M A G T A E G E G Q Q R H S Q 689
TCC TCT GGA GAA AAC ATG GCT GGG ACA GCT GAA GGT GAG GGT CAG CAA AGA CAC AGT CAG 2266

L K S S S K S Q A L M P I Q E P G T Q C 709
CTA AAA AGC TCA TCT AAA AGC CAG GCT CTA ATG CCA ATT CAA GAG CCT GGG ACT CAA TGT 2326

E L S Q N L Q N L Y G T P V F R P V L E 729
GAG CTC AGC CAG AAT CTT CAG AAT CTC TAT GGT ACC CCA GTA TTC AGG CCT GTT CTA GAG 2386

N S W L F P T R I G G N F N H V S L K A 749
AAC TCC TGG CTC TTT CCA ACC AGA ATT GGA GGT AAC TTT AAC CAT GTT TCC TTG AAA GCC 2446

S W V M G R P F G S E Q R P K W F H P L 769
TCC TGG GTT ATG GGC CGC CCC TTT GGG TCA GAG CAG AGG CCT AAG TGG TTC CAT CCT TTG 2506

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P F Q N A G A Q G R G K S F G I Q S F H 789
CCT TTT CAG AAT GCA GGG GCC CAG GGC CGA GGT AAA AGT TTT GGT ATT CAA TCC TTC CAT 2566

P Q I F Y S G E R F M K F S R V A R G C 809
CCC CAG ATA TTT TAT TCA GGT GAA AGA TTC ATG AAA TTT TCC AGA GTT GCT CGG GGA TGT 2626

H S N G T F G R L P R P I C Q H V Q A C 829
CAC TCG AAT GGA ACA TTT GGG AGA CTG CCA AGA CCC ATT TGT CAG CAT GTA CAG GCC TGC 2686

P E R P Q M M G T L E R S R A V A S K I 849
CCT GAG AGA CCA CAA ATG ATG GGA ACT CTT GAA AGG TCT AGG GCA GTA GCC TCC AAG ATA 2746

G H S Y S L D S Q P A R A V G K P W P Q 869
GGT CAC TCC TAT TCC CTG GAT TCA CAG CCA GCA AGA GCA GTA GGG AAG CCA TGG CCT CAG 2806

Q A C T R V T E L T E A T G K L I R T S 889
CAA GCT TGC ACC AGG GTA ACA GAG TTA ACT GAA GCA ACT GGA AAA CTG ATA AGA ACA TCC 2866

H I G K P H P Q S F Q P A A A T Q K L R 909
CAT ATT GGA AAG CCT CAC CCT CAG TCC TTT CAA CCA GCA GCA GCC ACA CAA AAA CTA AGA 2926

P A S Q Q G V Q M K T Q G G A S N P A L 929
CCT GCT TCT CAG CAA GGA GTC CAG ATG AAG ACA CAA GGT GGG GCT TCA AAT CCA GCT CTC 2986

Q I G S H P M C K S S Q F K S D Q S N P 949
CAA ATA GGG TCC CAT CCC ATG TGC AAG AGC TCT CAG TTC AAA TCC GAT CAG TCC AAC CCA 3046

S T V K H S Q P K P F H S V P S Q P K S 969
TCC ACA GTC AAA CAC TCC CAG CCT AAA CCC TTC CAT TCT GTG CCC TCT CAA CCT AAA TCC 3106

S Q T K S C Q S Q P S Q T K P S P C K S 989
TCT CAG ACA AAA TCC TGT CAG TCC CAG CCC TCC CAA ACT AAA CCT TCT CCA TGC AAA TCT 3166

T Q P K P S Q P W P P Q S K P S Q P R P 1009
ACT CAG CCT AAG CCA AGC CAG CCC TGG CCT CCC CAG TCT AAG CCT TCT CAG CCC AGA CCC 3226

P Q P K S S S T N P S Q A K A H H S K A 1029
CCT CAA CCT AAG TCA TCC TCA ACC AAT CCT TCA CAA GCT AAG GCA CAC CAC TCA AAA GCA 3286

G Q K R G G K H * 1038
GGG CAG AAG AGG GGA GGG AAG CAT TAA 3313

AGAGCTAACTCCAGAGATCTATAAAGCATATCCTTTACCCAGGCCATTCTCTATCATATAGTAAGCAGAAGAGTTGCCAT 3392

GAAAGTAAAAGACTACTGTTCATTAGCATGTAAAACAAAGAAAGATATACATGACCGAATTGGATATCTTTGTTTGTGTTG 3471

TTTGAGACAGAGTTTCACTCTTGTGTTGCCAGGCTGGAGTGCATGGCAGCATCTCGGCTCACCGCAACCTCTGCTTCCT 3550

GGCTTAAAGTGATTCTCCTGCCTCAGCCTCTCGAGTAGCTGGGATTACAGGCATGCACCACCACACCCAGCTAATTTTG 3629

TATTTTAGTAGAGGCAGGGTTTCTCCATGTTGGTCAGGCTGGTCTTGAACCTCCCGACCTCAGGTGATCCGCCCCACCTA 3708

GGCCTCTCAAAGTGTGGGATTACGTGTGTAAAGCCACAGTGCCCGAGCCGAATTGGATATCTTTAAGATATCTGTAAGT 3787

GTTATATCCCTAACCAAGAAGAAAAATATGAAAAATAATTAAGACTAGAATCAAGCAGTAGATAATTGAATCCAATCTTG 3866

GGTATTATTAGATAATGTATAACTTGCACCCAGGGAATGGGGTCTATGAGACAACCCCACTTGAGAAAGATGGGGTT 3945

AGGGTCTCTAATTGCAAAGTACTGTACAATAGGACGAAAGTTGCCTCTGTGTCTGAGAAAGTATCTTAGTTGTTGGCT 4024

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GCTCCAGAGGTATCTTTGTCAAAGCTTCTGGTTCAATATCAGCCACTGAGCAGATAACCCTGCTTATTTGGTGTGGTT 4103
AAATCAACTAGCTTCTGCTAATAGCCCCAATTTGCTTGAATGGGAAAACTCTCTCATTGACCCCTTATAGGTAGAAATA 4182
ATGAATTAACAACCAATAAAATTAATCATTGGCATTAAAAAAAAAAAAAAAAAAAAA 4244

57/58

CONSENSUS *->maederrlLkknrvriiesLgldvLdeiLdvLlekdvlnlkeeEkik
 +++ + ++ r++l+e+L+ d d +Ld L +++++ ++e E
CARD6 5 STP--SEIIERERKKLLEILQHD-PDSILDTLTSRRLISEEEYETLE 48
CONSENSUS ragakledDKarelvdslqrrgsqafdafidaledTgqsyLAdvLel<+
 + l + r l++ +q++g. + ++ f+ +l++ LA++ +l
CARD6 49 NVTDLLKK--SRKLLILVQKKGEATCQHFLKCLFS-TFPQLAAICGL 92

	- A - E S - G S E I I D Q H R X A L L A R V T E D P - D S L L D A L L S R D L I Majority																																												
	10										20										30										40														
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1	-	-	-	-	E	S	H	P	H	I	Q	L	L	K	S	N	R	E	L	I	V	T	H	R	N	T	-	Q	C	I	V	I	N	L	I	K	N	-	Y	F	hCARD4-CARD				
1	-	-	-	-	-	-	-	-	-	C	L	H	F	I	D	O	H	E	A	A	I	A	R	V	T	-	-	V	E	W	L	D	A	I	G	K	-	V	L	hCARD5-CARD					
1	-	-	-	-	-	-	-	-	-	C	-	H	F	V	D	O	H	E	A	A	I	A	R	V	T	-	-	V	I	G	V	L	D	A	I	H	G	S	-	V	L	hCARD5-CARD			
1	M	A	T	E	S	T	P	S	E	I	I	E	R	E	R	K	K	L	L	E	I	L	Q	H	D	P	-	D	S	I	L	E	T	I	T	S	F	R	L	I	hCARD6-CARD				
1	M	A	S	E	G	A	S	S	E	I	I	E	K	Q	P	T	K	L	L	S	V	L	Q	Q	D	P	-	D	S	I	L	E	T	I	T	S	F	R	L	I	hCARD6-CARD				
S E E D Y E A V E A E T T X L S K V R K L L I L V Q S K G E E T C K - F L K C L Majority																																													
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36	M	K	E	D	Y	E	L	A	S	T	K	P	T	R	T	S	K	V	R	Q	L	L	D	T	T	D	I	Q	G	E	-	-	-	-	I	A	H	V	I	hCARD3-CARD					
37	S	A	E	D	A	F	I	N	C	A	C	P	I	Q	P	D	K	V	R	K	I	I	D	I	V	O	S	K	G	E	E	V	S	E	F	F	I	-	Y	I	hCARD4-CARD				
32	T	D	E	Q	Y	Q	A	V	R	A	E	P	T	N	P	S	K	M	R	K	L	F	S	F	T	P	A	W	-	N	W	T	C	E	-	-	-	-	D	L	I	hCARD5-CARD			
31	T	E	G	Q	Y	Q	A	V	R	A	E	T	T	S	O	D	E	M	R	K	L	F	S	F	V	P	S	W	-	N	L	T	C	E	-	-	-	-	D	S	I	hCARD5-CARD			
40	S	E	E	E	Y	E	T	L	I	N	V	T	D	L	L	K	K	S	R	K	L	L	I	L	V	Q	K	K	G	E	A	T	C	Q	H	F	L	K	C	L	hCARD6-CARD				
40	S	E	E	E	Y	E	T	L	E	A	I	T	D	P	L	K	K	S	R	K	L	L	I	L	I	C	K	K	G	E	D	S	C	C	F	L	K	C	L	hCARD6-CARD					
L Q A L K D S A A Y L G L D P E V - - - - - L E - S Majority																																													
	90										100																																		
72	V	Q	K	L	K	D	N	K	O	-	M	G	I	Q	P	Y	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	I	L	hCARD3-CARD			
76	L	Q	Q	L	A	I	-	-	-	A	V	D	I	R	P	W	L																									hCARD4-CARD			
68	L	Q	A	L	R	E	S	Q	S	Y	L	V	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	E	R	S	hCARD5-CARD	
67	L	Q	A	L	K	E	I	H	P	Y	L	V	M	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	E	Q	S	hCARD5-CARD
80	F	S	T	F	P	Q	L	A	I	C	G	L	R	H	E	V	L																											hCARD6-CARD	
80	S	N	A	F	P	Q	S	A	S	T	L	G	L	K	Q	E	V	P	R	Q	G	T	G	E	V	V	E	V	S															hCARD6-CARD	

FIG. 31